

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 Seconds  
(without alignments)  
5753.635 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gaggtttaaatagattaaaac.....cccccaattgcagattttac 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_btg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

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13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	204	100.0	1659	6	E31042	E31042 Method for
2	204	100.0	1659	9	HSU32974	U32974 Human IAP-1
3	204	100.0	2086	9	BC032729	BC032729 Homo sapi
4	204	100.0	2404	6	AX429575	AX429575 Sequence
5	204	100.0	2540	6	AR103281	AR103281 Sequence
6	204	100.0	2540	6	AX412118	AX412118 Sequence
7	204	100.0	2540	9	HSU45880	U45880 Human X-11n
8	204	100.0	3000	6	AX412131	AX412131 Sequence
9	204	100.0	5232	6	AR106397	AR106397 Sequence
10	204	100.0	5232	6	AR116699	AR116699 Sequence
11	204	100.0	13391	9	HSU315G1	U315G1 Human DNA
12	204	100.0	201197	2	HS424J12	HS424J12 Homo sapien
13	172	84.3	2100	6	AX412124	AX412124 Sequence
14	172	84.3	2691	6	AR106400	AR106400 Sequence
15	172	84.3	2691	6	AR116702	AR116702 Sequence
16	172	84.3	2691	10	MMU88990	U88990 Mus musculu
17	170.4	83.5	1988	10	MMU36842	U36842 Mus musculu
18	168.8	82.7	2032	10	AF304333	AF304333 Rattus no
19	168.8	82.7	2468	10	AB033366	AB033366 Rattus no
20	168.8	82.7	3032	10	AF304334	AF304334 Rattus no
21	167.2	82.0	1491	10	AF183429	AF183429 Rattus no
22	156.8	76.9	187568	9	AF002967	AF002967 Homo sapi
23	153.4	75.2	7990	6	AX281265	AX281265 Sequence
24	153.4	75.2	7990	6	AX345060	AX345060 Sequence
25	129.4	63.4	7990	6	AX281266	AX281266 Sequence
26	129.4	63.4	7990	6	AX345061	AX345061 Sequence
27	123	60.3	179491	2	AC020673	AC020673 Homo sapi
28	111.4	54.6	1740	5	AF451854	AF451854 Gallus ga
29	68.4	33.5	1758	6	AX370787	AX370787 Sequence
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31	68.4	33.5	2032	9	AF420440	AF420440 Homo sapi
32	68.4	33.5	4993	9	AF164682	AF164682 Homo sapi
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35	68.4	33.5	165662	9	AC092070	AC092070 Homo sapi
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37	67	32.8	9960	5	AF311289	AF311289 Gallus ga
38	66.4	32.5	1946	5	AF442500	AF442500 Danio rer
39	66.4	32.5	163882	2	AL627325	AL627325 Danio rer
40	63.8	31.3	2667	5	GGU27466	U27466 Gallus gall
41	63.6	31.2	1218	5	AF439767	AF439767 Danio rer
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43	62.2	30.5	2474	6	AX412126	AX412126 Sequence
44	62.2	30.5	2676	6	AR106401	AR106401 Sequence
45	62.2	30.5	2676	6	AR116703	AR116703 Sequence

# ALIGNMENTS

RESULT 1  
E31042  
LOCUS E31042 Method for screening substance inhibiting binding to XIAP. linear PAT 18-JUN-2001  
DEFINITION E31042  
ACCESSION E31042  
VERSION E31042.1 GI:13017307  
KEYWORDS JP 1999326328-A/2.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1659)  
AUTHORS Kunihiro,M.  
TITLE Method for screening substance inhibiting binding to XIAP  
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;  
KUNIHIO MATSUMOTO

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COMMENT OS Unidentified
PN JP 1999326328-A/2
PD 26-NOV-1999
PF 13-MAY-1998 JP 1998130378
PR KUNITHIRO MATSUKOTO
PI G01N33/536
PC G01N33/566 A61K38/00 A61K38/00 A61K38/00 A61K38/22,
PC A61K39/395
PC A61K45/00 A61K45/00 A61K45/00 C07K7/06 C07K7/08 C07K14/47 PC
PC G01N33/536
PC G01N33/536 G01N33/536//C12N15/09 C12P21/08 A61K37/02,
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CC Topology: Linear;
FH Key Location/Qualifiers
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LOCUS Human IAP-like protein ILP mRNA, complete cds.
DEFINITION U32974
ACCESSION U32974
VERSION U32974.1 GI:1016687
KEYWORDS apoptosis; ring finger; zinc finger.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1659)
AUTHORS Duckett,C.S. and Thompson,C.B.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3e-50;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 157 GAGTTAATAGATTAATAAATCTTTGCTAATTTTCCAAAGTGGTAGTCCCTGTTTCAGCATCA 216
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DB 277 TGTCATGACGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTGGAAGACACAGGAAA 336
QY 181 GTATCCCAAAATTCAGATTATC 204
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DB 337 GTATCCCAAAATTCAGATTATC 360

RESULT 3
BC032729 2086 bp mRNA linear PRI 27-JUN-2002
LOCUS Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369
DEFINITION IMAGE:5532247, mRNA, complete cds.
ACCESSION BC032729
VERSION BC032729.1 GI:21619763
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2086)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov

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Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: nisc.mc@hghri.nih.gov  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
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Db 334 GTATCCCCAAATTCGAGATTATC 357  
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AX429575  
LOCUS

DEFINITION Sequence 38 from Patent WO0226820.  
ACCESSION AX429575  
VERSION AX429575.1 GI:21540833  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,  
Reinhardt, M.W. and Zisman, S.  
TITLE Transgenic drosophila melanogaster expressing beta anyloid  
JOURNAL Patent: WO 0226820-A 38 04-APR-2002;  
NOVARTIS ERFINO VERWALT GMBH (AT)  
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LOCUS

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ACCESSION AR103281  
VERSION AR103281.1 GI:12814869  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2540)  
AUTHORS Bennett, C.Frank., Ackermann, E.J. and Cowser, L.M.  
TITLE Antisense modulation of x-linked inhibitor of apoptosis expression  
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
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 VERSION AX412118.1 GI:21444581  
 KEYWORDS  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
 TITLE Antisense lbp nucleic acids and uses thereof  
 JOURNAL Patent: WO 0226968-A 218 04-APR-2002;  
 University of Ottawa (CA); Aegera Therapeutics Inc. (CA)  
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RESULT 7  
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 LOCUS  
 DEFINITION Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete  
 cds.  
 ACCESSION U45880  
 VERSION U45880.1 GI:1184319  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2540)  
 AUTHORS Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,  
 Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., Mackenzie, A.  
 and Korneluk, R.G.  
 TITLE Suppression of apoptosis in mammalian cells by NAIP and a related  
 family of IAP genes  
 JOURNAL Nature 379 (6563), 349-353 (1996)

96149249  
 8552191  
 2 (bases 1 to 2540)  
 Baird, S.D.  
 Direct Submission  
 Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of  
 Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1,  
 Canada  
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 /codon\_start=1  
 /evidence=experimental  
 /product="X-linked inhibitor of apoptosis protein"  
 /protein\_id="AAC50373.1"  
 /translation="MTNFEFGSKTCVPADINKKEEFVEEFNRKLTNFANFGSPVSA  
 STLARAGLTGEGDVTVCFSCHAAVDWYGDVAVGRHRKVSFNCRFINGFYLENSA  
 TOSTNSGIQNGQYKVENYVLAGSRDHFALDRPSETHADYLLRTGVVDISDTIYPRNPAM  
 YCEEARLKSQNMWPDYAHLPRELASAGLYTIGDQVCCGCKLKNWPCDRAWS  
 EHRHFPNCFVFLGNLNIRSDVSSDRNFPNLPNPSMADYEARLFTGTWI  
 YSVNKEQLARAGFYALGEGDKVCFHCGGGLTDWKPSEDWPEHAKWYPGCKYLDLEQK  
 GOEYINNHLTHSLECLVTRTEKTPSLTRIDDTIFQNPVQEARIRMGFSFKDIIKI  
 MEERKIQISGNYKSLVLAADLVNAQKDSMODESSQTSLOKEISTEOLRRRLQBEKLC  
 KICMDRNIAIVFVPCGHLVTCCKCAEAVDKPCMCYTVITTFQKIFMS"  
 108..309  
 /note="encodes BIR1 (Baculovirus IAP Repeat)"  
 520..723  
 /note="encodes BIR2"  
 826..1020  
 /note="encodes BIR3"  
 1381..1485  
 /note="encodes Ring Zinc Finger"  
 BASE COUNT 781 a 415 c 571 g 773 t  
 ORIGIN

Query Match 100.0%; Score 204; DB 9; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-50;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTTTAAATAGATTAAACACTTTTGCCTAATTTCCAAAGTGTAGTCTGTTTCAGCATCA 60  
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 Db 109 GAGTTTAAATAGATTAAACACTTTTGCCTAATTTCCAAAGTGTAGTCTGTTTCAGCATCA 168  
 |||||  
 Qy 61 ACATGGCAGCAGCAGGTTTCTTTATCTACTGTGTAAGAGATACCGTCCGCTGCTTAGT 120  
 |||||  
 Db 169 ACATGGCAGCAGCAGGTTTCTTTATCTACTGTGTAAGAGATACCGTCCGCTGCTTAGT 228  
 |||||  
 Qy 121 TGTATGAGCTGTAGATAGTGGCAATATGAGACTCAGCAGTTGGAAGACACAGGAAA 180  
 |||||  
 Db 229 TGTATGAGCTGTAGATAGTGGCAATATGAGACTCAGCAGTTGGAAGACACAGGAAA 288  
 |||||  
 Qy 181 GTATCCCCAAATTCAGATTATC 204  
 |||||  
 Db 289 GTATCCCCAAATTCAGATTATC 312  
 |||||

RESULT 8  
 AX412131  
 LOCUS  
 DEFINITION Sequence 231 from Patent WO0226968.  
 ACCESSION AX412131  
 VERSION AX412131.1 GI:21444588  
 KEYWORDS  
 SOURCE human.  
 AX412131  
 Sequence 231 from Patent WO0226968.  
 PAT 14-JUN-2002



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
TITLE Antisense iap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 231 04-APR-2002;  
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)

FEATURES  
source Location/Qualifiers  
1..3000  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 974 a 452 c 601 g 973 t  
ORIGIN

Query Match 100.0%; Score 204; DB 6; Length 3000;  
Best Local Similarity 100.0%; Pred. No. 3.1e-50;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATTAATAAAGCTTTGCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCA 60  
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QY 61 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120  
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Db 825 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 884  
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QY 121 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180  
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Db 885 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 944  
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QY 181 GTATCCCAAAATTCAGATTATC 204  
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Db 945 GTATCCCAAAATTCAGATTATC 968  
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RESULT 9  
LOCUS AR106397 5232 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 3 from patent US 6107041.  
ACCESSION AR106397  
VERSION AR106397.1 GI:12820927  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL Patent: US 6107041-A 3 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..5232  
/organism="unknown"  
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others  
ORIGIN

Query Match 100.0%; Score 204; DB 6; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 3.3e-50;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATTAATAAAGCTTTGCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCA 60  
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Db 109 GAGTTTAAATAGATTAATAAAGCTTTGCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCA 168  
|||||

QY 61 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120  
|||||  
Db 169 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 228  
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QY 121 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180  
|||||  
Db 229 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 288  
|||||

QY 181 GTATCCCAAAATTCAGATTATC 204  
|||||  
Db 289 GTATCCCAAAATTCAGATTATC 312  
|||||

RESULT 11  
LOCUS HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000  
DEFINITION Human DNA sequence from clone Rpl-315G1 on chromosome Xq24-25. Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene, ESTs, SPSS, GSs and a putative CpG island, complete sequence.

ACCESSION AL121601  
VERSION AL121601.13 GI:7159760  
KEYWORDS HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 133391)  
AUTHORS Direct Submission  
TITLE Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
JOURNAL requests: clonequery@sanger.ac.uk  
COMMENT On Mar 6, 2000 this sequence version replaced gi:6983378. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

QY 181 GTATCCCAAAATTCAGATTATC 204  
|||||  
Db 289 GTATCCCAAAATTCAGATTATC 312  
|||||

RESULT 10  
LOCUS AR116699 5232 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6133437.  
ACCESSION AR116699  
VERSION AR116699.1 GI:14097021  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..5232  
/organism="unknown"  
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others  
ORIGIN

Query Match 100.0%; Score 204; DB 6; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 3.3e-50;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATTAATAAAGCTTTGCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCA 60  
|||||  
Db 109 GAGTTTAAATAGATTAATAAAGCTTTGCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCA 168  
|||||

QY 61 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120  
|||||  
Db 169 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 228  
|||||

QY 121 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180  
|||||  
Db 229 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 288  
|||||

QY 181 GTATCCCAAAATTCAGATTATC 204  
|||||  
Db 289 GTATCCCAAAATTCAGATTATC 312  
|||||

RESULT 11  
LOCUS HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000  
DEFINITION Human DNA sequence from clone Rpl-315G1 on chromosome Xq24-25. Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene, ESTs, SPSS, GSs and a putative CpG island, complete sequence.

ACCESSION AL121601  
VERSION AL121601.13 GI:7159760  
KEYWORDS HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 133391)  
AUTHORS Direct Submission  
TITLE Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
JOURNAL requests: clonequery@sanger.ac.uk  
COMMENT On Mar 6, 2000 this sequence version replaced gi:6983378. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information by the WormPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>  
RPI-315G1 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pCYPAC2

This sequence is the entire insert of clone RPI-315G1 The true right end of clone RP6-30A23 is at 100 in this sequence.

#### FEATURES

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1. 133391
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   /db_xref="taxon:9606"
   /chromosome="X"
   /map="q24-q25"
   /clone="RPI-315G1"
   /clone_lib="RPCI-1"
   complement(3738..4224)
   /note="match: GSS: Em:AQ885645"
   complement(4112..4623)
   /note="match: GSS: Em:AQ623859"
   4617..5326
   /note="match: GSS: Em:AQ740042"
   4624..4824
   /note="match: GSS: Em:AQ587673"
   4828..5111
   /note="match: GSS: Em:AQ587673"
   complement(6712..7417)
   /gene="dJ315G1.1"
   complement(6712..7417)
   /gene="dJ315G1.1"
   /note="dJ315G1.1 (PDZ (DHR, GLGF) domain protein
   pseudogene)
   match: ESTs: Em:AW369746
   match: proteins: Tr:O9Y510 Tr:O14911 Tr:Q9Z101 Tr:O18129
   Tr:O97111"
   /pseudo
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##### misc\_feature

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/note="match: GSS: Em:AQ885645"
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##### misc\_feature

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/note="match: GSS: Em:AQ623859"
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##### misc\_feature

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##### misc\_feature

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/note="match: GSS: Em:AQ587673"
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##### gene

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/note="match: GSS: Em:AQ587673"
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##### CDS

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/gene="dJ315G1.1"
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##### CDS

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/note="dJ315G1.1 (PDZ (DHR, GLGF) domain protein
pseudogene)
match: ESTs: Em:AW369746
match: proteins: Tr:O9Y510 Tr:O14911 Tr:Q9Z101 Tr:O18129
Tr:O97111"
/pseudo
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##### gene

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/codon_start=1
/evidence=not_experimental
13544..36179
/gene="API3"
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##### mRNA

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28615..28815,35110..36179)
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/product="dJ315G1.2 (apoptosis inhibitor 3 (XIAP, HILP))"
/note="match: CDNAS: Em:AB033366 Em:U88990 Em:U32974
Em:U45880 Em:U36842
match: ESTs: Em:HSCZOG051 Em:AI628066 Em:AA295472
Em:AI598959 Em:AI418337 Em:AI277821 Em:HSCZOG052
Em:AA987840"
/evidence=not_experimental
join(13785..14661,16741..16840,19360..19438,20853..20895,
28615..28815,35110..35303)
/gene="API3"
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##### CDS

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/note="match: proteins: Tr:O57319 Sw:P98170 Sw:Q90660
Sw:Q13490 Sw:Q60989 Sw:Q62210"
/codon_start=1
/evidence=not_experimental
/product="dJ315G1.2 (apoptosis inhibitor 3 (XIAP, HILP))"
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/db_xref="GI:8744934"
/translation="MTNPFSGSKTCVPADLNKKEEFVEEENRLKTFANFPGSGSPVSA
STLAAGLFTYEGEDTVRCFCHAAVDWQYGDGAVGRHKVSPNCRINGFIYENSA
TQSNKIQNGQYKVENYVIGSRDHFALDRPSETHADYLLRTQGVVDISDTIYPRNPAM
YSEARLKSFQWPDYALHTPRELASAGLYVTGIGDQVQCFCGKGLKNWPCDRAMS
EHRHFEPCFVLGNLNIRSEDAVSSDRNPSTNLPRNPSMADYEARLFTFTGLI
YSVNEQLARAGFYALSGDKVKCFHCGGLTDMKPSDPNEQHNKWPYGGKYLLEQK
QYETINHLTHLSLECLRTERTPTSLRITDITFQNPVQGAIRMGFSFKDKLKKI
MEERKIQSGSNYKLEVLADLVNAQKDSQDESSQTSLOKEISTEELRLQAEKLC
KICMDRNTAIVFVPCGHLVTKQCAEAVDKCPMGVYTVTFKQIFMS"
16117..16170
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complement(join(16759..16840,19360..19438,20853..20895,
28618..28815))
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/note="90 copies 2 mer ta 73% conserved"
complement(28616..28815)
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complement(29161..29662)
/note="match: GSS: Em:AQ719253"
29663..29811
/gene="API3"
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31721..31780
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complement(35122..35394)
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35386..35721
/gene="API3"
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complement(40019..40354)
/note="match: STS: Em:AA017266"
complement(40058..40218)
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40354..40395
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complement(41858..42269)
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/note="match: STS: Em:L77256"
55942..56315
/note="match: STS: Em:L40935"
56488..56535
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/note="match: GSS: Em:AQ485834 Em:AQ540857"
join(69586..69636,70004..70193)
/note="match: GSS: Em:B64443"
complement(69632..69815)
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complement(69632..69793)
/note="match: GSS: Em:AQ380019"
complement(69645..69791)
/note="match: GSS: Em:AQ405293"
69653..69814
/note="match: GSS: Em:AQ383553"
complement(69661..69806)
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complement(69661..69771)
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69685..69792
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/misc_feature      /note="match: GSS: Em:AQ347249"
complement(69921..70100)
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complement(69956..70137)
/misc_feature      /note="match: GSS: Em:AQ802964"
69958..70287
/note="match: STS: Em:G42844"
69958..70201
/note="match: GSS: Em:AQ166728"
69958..70109
/note="match: GSS: Em:AQ479649"
complement(69964..70254)
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complement(69964..70177)
/misc_feature      /note="match: GSS: Em:AQ390824"
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/note="match: GSS: Em:AQ523288"
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70749..70962
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/note="32 copies 2 mer tt 71% conserved"
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Query Match 100.0%; Score 204; DB 9; Length 13391;

Best Local Similarity 100.0%; Pred. No. 4.1e-50;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GAGTTTATAGATTTAAACCTTTCTTATCTGTTGAGGATGAGTCCGTTTCAGCATCA 60
Db 13860 GAGTTTATAGATTTAAACCTTTCTTATCTGTTGAGGATGAGTCCGTTTCAGCATCA 13919
Qy 61 ACATGCGCAGCAGCGGTTTCTTATCTGTTGAGGATGAGTCCGTTTCAGCATCA 120
Db 13920 ACATGCGCAGCAGCGGTTTCTTATCTGTTGAGGATGAGTCCGTTTCAGCATCA 13979
Qy 121 TGTCATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
Db 13980 TGTCATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 14039
Qy 181 GTATCCCAAAATGCGAGATTATC 204
Db 14040 GTATCCCAAAATGCGAGATTATC 14063

```

```

RESULT 12
HS424J12      201197 bp      DNA      linear      HTG 10-JUL-2001
LOCUS      Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN
DEFINITION      PROGRESS ***, 15 unordered pieces.
ACCESSION      Z82207
VERSION      Z82207.3
KEYWORDS      HTG; HTGS-PHASE1; HTGS-CANCELLED.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 201197)

```

```

REFERENCE      Direct Submission
AUTHORS      Grahnam,D.
TITLE      Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL      CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerquest@sanger.ac.uk
COMMENT      On Jan 22, 2001 this sequence version replaced gi:10045116.
***** Genome Center

```

Center: Sanger Centre  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
----- Project Information  
Center project name: dJ424J12  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: M13; M7815; 74% of reads  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Chemistry: Dye-terminator ABI; 96% of reads  
Chemistry: Dye-primer-amersham; 2% of reads  
Chemistry: Dye-primer Big Dye; 0% of reads  
Consensus quality: 194333 bases at least Q40  
Consensus quality: 196512 bases at least Q30  
Consensus quality: 198047 bases at least Q20  
Insert size: 199797; sum-of-contigs  
Quality coverage: 6.87x in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 15 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

```

* 1 4154: contig of 4154 bp in length
* 4155 4254: gap of 100 bp
* 4255 18703: contig of 14449 bp in length
* 18704 18803: gap of 100 bp
* 18804 20941: contig of 2138 bp in length
* 20942 21041: gap of 100 bp
* 21042 34907: contig of 13866 bp in length
* 34908 35012: gap of 105 bp
* 35013 37508: contig of 2496 bp in length
* 37509 37608: gap of 100 bp
* 37609 52739: contig of 15131 bp in length
* 52740 52839: gap of 100 bp
* 52840 56933: contig of 4094 bp in length
* 56934 57033: gap of 100 bp
* 57034 88245: contig of 31212 bp in length
* 88246 88346: gap of 101 bp
* 88347 93386: contig of 5040 bp in length
* 93387 93486: gap of 100 bp
* 93487 123956: contig of 30470 bp in length
* 123957 124056: gap of 100 bp
* 124057 147917: contig of 23861 bp in length
* 147918 148017: gap of 100 bp
* 148018 176236: contig of 28219 bp in length
* 176237 176336: gap of 100 bp
* 176337 187128: contig of 10792 bp in length
* 187129 187228: gap of 100 bp
* 187229 190824: contig of 3596 bp in length
* 190825 190939: gap of 135 bp
* 190960 201197: contig of 10238 bp in length.

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#### FEATURES

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/db_xref="taxon:9606"
/chromosome="X"
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fragment_chain:1"
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18804..20941
/note="assembly_fragment:03282
fragment_chain:2"

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/note="assembly\_fragment:03624  
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35008..37508  
/note="assembly\_fragment:00340"  
37609..52739  
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52840..56933  
/note="assembly\_fragment:01287.0"  
57034..88245  
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88346..93386  
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93487..123956  
/note="assembly\_fragment:03234"  
124057..147917  
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148018..176236  
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176337..187128  
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190925..201197  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 42632 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 42691  
QY 61 ACACGTGGCAGCAGCGGGTTCTTTATCTGCTGAGGAGATACCGTGGGTGCTTTAGT 120  
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QY 121 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 180  
|||||  
Db 42752 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 42811  
QY 181 GTATCCCCAAATTCGAGATTATC 204  
|||||  
Db 42812 GTATCCCCAAATTCGAGATTATC 42835

RESULT 13  
LOCUS AX412124 2100 bp DNA linear PAT 15-JUN-2002  
DEFINITION Sequence 224 from Patent WO0226969.  
ACCESSION AX412124  
VERSION AX412124.1 GI:21444584  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.  
TITLE Antisense iap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 224 04-APR-2002;  
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)  
FEATURES  
Source  
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/db\_xref="taxon:10090"  
BASE COUNT 615 a 417 c 482 g 586 t  
ORIGIN

Query Match 84.3%; Score 172; DB 6; Length 2100;  
Best Local Similarity 90.2%; Pred. No. 1.1e-40;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60  
|||||  
Db 202 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 261  
QY 61 ACACGTGGCAGCAGCGGGTTCTTTATCTGCTGAGGAGATACCGTGGGTGCTTTAGT 120  
|||||  
Db 262 ACATTTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 321  
QY 121 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 180  
|||||  
Db 322 TGTCTATGCGGCAATAGATAGATGCGCAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 381  
QY 181 GTATCCCCAAATTCGAGATTATC 204  
|||||  
Db 382 ATATCCCCAAATTCGAGATTATC 405

RESULT 14  
LOCUS ARI06400 2691 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6107041.  
ACCESSION ARI06400  
VERSION ARI06400.1 GI:12820930  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2691)  
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..2691  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 84.3%; Score 172; DB 6; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 1.2e-40;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60  
|||||  
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QY 61 ACACGTGGCAGCAGCGGGTTCTTTATCTGCTGAGGAGATACCGTGGGTGCTTTAGT 120  
|||||  
Db 807 ACATTTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 866  
QY 121 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 180  
|||||  
Db 867 TGTCTATGCGGCAATAGATAGATGCGCAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 926  
QY 181 GTATCCCCAAATTCGAGATTATC 204  
|||||  
Db 927 ATATCCCCAAATTCGAGATTATC 950

RESULT 15  
LOCUS ARI16702 2691 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 9 from patent US 6133437.  
ACCESSION ARI16702  
VERSION ARI16702.1 GI:14097024  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (Bases 1 to 2691)  
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 613437-A 9 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..2691  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN  
Query Match 84.3%; Score 172; DB 6; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 1.2e-40;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAATAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCA 60  
Db 747 GAGTTTAATAGATTAATAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCA 806  
Qy 61 ACACGGGCACGAGCAGGCTTTTACTGTTGTAAGGAGATACCGTGGGTGCTTTAGT 120  
Db 807 ACATTGGGCGGAGCTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866  
Qy 121 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180  
Db 867 TGTCATGGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 926  
Qy 181 GTATCCCCCAATTGCAGATTATC 204  
Db 927 ATATCCCCCAATTGCAGATTATC 950

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
3369.223 Million cell updates/sec

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Scoring table: IDENTITY\_NUC

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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2:	/SID2/cgdata/geneseq/geneseqn-emb1/NA1981.DAT.*	204	100.0	2404	24	AAK99405 DNA of APP related
3:	/SID2/cgdata/geneseq/geneseqn-emb1/NA1982.DAT.*	204	100.0	2540	18	AAK70836 Human apoptosis in
4:	/SID2/cgdata/geneseq/geneseqn-emb1/NA1983.DAT.*	204	100.0	2540	21	AAK64901 Human X-linked inh
5:	/SID2/cgdata/geneseq/geneseqn-emb1/NA1984.DAT.*	204	100.0	2540	24	ABK93869 Human cDNA encodin
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9:	/SID2/cgdata/geneseq/geneseqn-emb1/NA1988.DAT.*	172	84.3	2100	24	ABK93872 Mouse cDNA encodin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	204	100.0	1659	21	AAZ48862 Human XIAP coding
2	204	100.0	2404	24	AAK99405 DNA of APP related
3	204	100.0	2540	18	AAK70836 Human apoptosis in
4	204	100.0	2540	21	AAK64901 Human X-linked inh
5	204	100.0	2540	24	ABK93869 Human cDNA encodin
6	204	100.0	3000	24	ABK93875 Human cDNA encodin
7	204	100.0	5232	19	AAV55038 Human XIAP coding
8	172	84.3	2100	18	AAK70839 Mouse apoptosis in
9	172	84.3	2100	24	ABK93872 Mouse cDNA encodin

10	172	84.3	2691	19	AAV55041 Murine XIAP coding
11	170.4	83.5	1988	18	AAK72710 Mouse inhibitor of
12	153.4	75.2	7990	24	ABL54307 Chemically treated
13	153.4	75.2	7990	24	ABL32158 Human immune syste
14	129.4	63.4	7990	24	ABL34308 Chemically treated
15	129.4	63.4	7990	24	ABL32159 Human immune syste
16	68.4	33.5	1559	24	ABK13197 Human testes speci
17	68.4	33.5	1758	24	ABK14677 Human inhibitor of
18	68.4	33.5	1758	24	ABK14678 Human IAP-like pro
19	68.4	33.5	4993	22	AAK03581 Mouse apoptosis in
20	62.2	30.5	2416	18	AAK70841 Mouse cDNA encodin
21	62.2	30.5	2416	24	ABK93874 Mouse apoptosis in
22	62.2	30.5	2474	18	AAK70840 Mouse cDNA encodin
23	62.2	30.5	2474	24	ABK93873 Murine HIAP-1 codi
24	62.2	30.5	2676	19	AAV55042 Murine c-IAP, Mus
25	62.2	30.5	2862	18	AAK61592 Murine HIAP-2 codi
26	62.2	30.5	3151	19	AAV55043 AmEPV baculovirus-
27	58.2	28.5	794	24	ABL55643 Human apoptosis in
28	58.2	28.5	50000	24	ABL55643 Human apoptosis in
29	56	27.5	2666	18	AAK70837 Human cDNA encodin
30	56	27.5	2676	24	ABK93870 Human inhibitor of
31	56	27.5	3076	18	AAK72712 Human cellular inh
32	56	27.5	3076	20	AAZ41005 Breast cancer rela
33	56	27.5	3076	20	AAZ22096 Lung cancer relate
34	56	27.5	3076	24	ABL62746 Human HIAP-1 codin
35	56	27.5	3076	24	ABL66325 Human cDNA encodin
36	56	27.5	6669	19	AAV55039 Human colon cancer
37	56	27.5	6669	24	ABK93876 Human apoptosis in
38	55.8	27.4	549	24	ABQ60576 Human cDNA encodin
39	55.8	27.4	2580	18	AAK70838 Human apoptosis in
40	55.8	27.4	2580	24	ABK93871 Human cDNA encodin
41	55.8	27.4	2589	18	AAK61590 Human inhibitor of
42	55.8	27.4	3532	18	AAK72711 Human cellular inh
43	55.8	27.4	3532	20	AAZ22143 Gene #3355 used to
44	55.8	27.4	3532	24	ABN96857 Human HIAP-2 codin
45	55.8	27.4	3732	19	AAV55040

#### ALIGNMENTS

#### RESULT 1

AAZ48862  
ID AAZ48862 standard; cDNA; 1659 BP.

XX AAZ48862;

XX 24-MAR-2000: (first entry)

DT Human XIAP coding sequence.

DE Human XIAP coding sequence.

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;

KW transforming growth factor-beta activated kinase 1; monocyte migration;

KW TAK1 binding protein 1; extracellular matrix protein production;

KW cell growth inhibitor; beta-amyloid protein deposition;

KW immunosuppression; Transforming growth factor-beta; ds.

XX Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-0130378.

XX 13-MAY-1998; 98JP-0130378.

XX (MATS/) MATSUMOTO K.

XX WPI; 2000-078337/07.

XX P-PSDB; AAY59451.

XX Screening a substance which inhibits combination of the X-linked

PT

PT Inhibitor of apoptosis protein  
PS Disclosure; Page 28-30; 43pp; Japanese.  
XX  
XX This sequence encodes the human XIAP protein.  
CC The invention relates to a method for screening a substance inhibiting  
CC the formation of a complex between XIAP and TAB1, in which X-linked  
CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
CC activated kinase 1 (TAK1) binding protein 1 (TAB1) and a substance to be  
CC tested are contacted with each other and then the presence or formation  
CC of a complex between XIAP and TAB1 is detected. The substance can be used  
CC as a drug for extracellular matrix protein production enhancement, cell  
CC growth inhibition, monocyte migration, physiologically active substance  
CC induction, immunosuppression, and beta-amyloid protein deposition. A  
CC substance inhibiting the formation of a complex between TAB1 and XIAP as  
CC well as between XIAP and TGF-beta (transforming growth factor-beta) type  
CC I and/or type II receptor is useful as a drug.  
XX  
SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
Query Match 100.0%; Score 204; DB 21; Length 1659;  
Best Local Similarity 100.0%; Pred. No. 8.5e-58;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAACTGGTAGTCTCTGTTTCAGCATCA 60  
Db 157 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAACTGGTAGTCTCTGTTTCAGCATCA 216  
Qy 51 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGTTGAGGAGATACCGTGGTGTCTTTAGT 120  
Db 217 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGTTGAGGAGATACCGTGGTGTCTTTAGT 276  
Qy 121 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180  
Db 277 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 336  
Qy 181 GTATCCCCAAATTCAGATTATC 204  
Db 337 GTATCCCCAAATTCAGATTATC 360  
RESULT 2  
AAK99405  
ID AAK99405 standard; DNA; 2404 BP.  
XX  
XX AAK99405;  
XX  
XX 27-JUN-2002 (first entry)  
XX  
XX DNA of APP related human homologue hCP35211.  
XX  
XX Neuroprotective; nontropic; transgenic fly; Alzheimer's disease; Abeta;  
KW amyloid precursor protein; tissue-specific expression control; human APP;  
KW APP pathway modulator; gene therapy; gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 692..1528  
FT CDS  
FT /tag= a  
FT /product= "Protein of human homologue hCP35211"  
FT /note= "No start codon"  
XX  
XX WO200226820-A2.  
XX  
XX 04-APR-2002.  
XX  
XX 01-OCT-2001; 2001WO-EP11345.  
XX  
XX 29-SEP-2000; 2000US-236893P.  
PR 14-JUN-2001; 2001US-298309P.  
XX  
XX (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;  
PI Reinhardt MWM, Zusman S;  
XX  
XX WPT; 2002-315796/35.  
DR P-PSDB; AAO20511.  
XX  
XX New transgenic fly, containing DNA encoding an Abeta portion of human  
PT APP, useful for identifying agents which modulate the APP pathway and  
PT which can be used to treat Alzheimer's disease  
XX  
XX Example 4; Page 111; 129pp; English.  
XX  
XX The invention relates to a transgenic fly whose genome comprises DNA  
CC encoding a polypeptide having the Abeta portion of human amyloid  
CC precursor protein (APP), fused to a signal sequence. The DNA sequence  
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in  
CC the specification. The DNA sequence is operably linked to a tissue-  
CC specific expression control sequence. Expression of the sequence gives  
CC the fly an altered phenotype. The purpose of the invention is for  
CC identifying agents that inhibit or promote the expression and/or function  
CC of genes or encoded polypeptides which modify the APP pathway. The agent  
CC is a compound, triple helix DNA, antisense oligonucleotide, double  
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
CC to treat conditions such as Alzheimer's disease. The agent can be used as  
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence  
CC represents the DNA of the APP related human homologue hCP35211.  
XX  
SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;  
Query Match 100.0%; Score 204; DB 24; Length 2404;  
Best Local Similarity 100.0%; Pred. No. 1e-57;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAACTGGTAGTCTCTGTTTCAGCATCA 60  
Db 109 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAACTGGTAGTCTCTGTTTCAGCATCA 168  
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGTTGAGGAGATACCGTGGTGTCTTTAGT 120  
Db 169 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGTTGAGGAGATACCGTGGTGTCTTTAGT 228  
Qy 121 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180  
Db 229 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 288  
Qy 181 GTATCCCCAAATTCAGATTATC 204  
Db 289 GTATCCCCAAATTCAGATTATC 312  
RESULT 3  
AAK70836  
ID AAK70836 standard; cDNA; 2540 BP.  
XX  
XX AAK70836;  
XX  
XX 02-SEP-1997 (first entry)  
XX  
XX Human apoptosis inhibitor xiap cDNA.  
DE  
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
KW ischaemia; myocardial infarction; stroke;  
KW reperfusion injury; toxin-induced liver disease; gene therapy;  
KW diagnosis; ds.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 34..1527  
FT CDS  
FT /tag= a

```

XX PN W09706255-A2.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-IB01022.
XX PR 22-DEC-1995; 95US-0576956.
XX PR 04-AUG-1995; 95US-0511485.
XX PA (UTOT-) UNIV OTTAWA.
XX PI Baird S, Korneluk RG, Liston P, Mackenzie AB;
XX DR WPI: 1997-154262/14.
XX DR P-PSDB; AAW19581.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX PT of susceptibility to apoptotic disease
XX PS Claim 12; Page 67-68; 21pp; English.
XX CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
XX CC hiap-2 genes (AAW70836-41) respectively code for a new class of
XX CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
XX CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
XX CC human foetal brain Zapfi cDNA library using an X-linked sequence
XX CC tag site that shows strong homology with the conserved ring zinc
XX CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
XX CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
XX CC to express IAP polypeptides in cells and animals to inhibit
XX CC apoptosis, and as primers and probes to identify and isolate
XX CC additional IAP genes, as well as in methods for treating diseases
XX CC and disorders involving apoptosis (anti-apoptotic gene therapy).
XX SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;

Query Match 100.08; Score 204; DB 18; Length 2540;
Best Local Similarity 100.08; Pred. No. 1e-57;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
DB 109 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168

QY 61 ACACGTGGCAGCAGCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGGGTGCTTTTACT 120
DB 169 ACACGTGGCAGCAGCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGGGTGCTTTTACT 228

QY 121 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTTGAAGACACAGGAAA 180
DB 229 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTTGAAGACACAGGAAA 288

QY 181 GTATCCCCAAATTCAGATTATC 204
DB 289 GTATCCCCAAATTCAGATTATC 312

RESULT 4
AAA64901
ID AAA64901 standard; DNA; 2540 BP.
XX: AAA64901;
AC:
XX:
XX:
DT 07-NOV-2000 (first entry)
DE Human X-linked inhibitor of apoptosis DNA.
XX X-linked inhibitor of apoptosis; XIAP; hiLP; MIHA; U45880;
KW antisense; antiinflammatory; cytostatic; tumour; ds.
XX Homo sapiens.
OS

```

```

XX FH Key Location/Qualifiers
XX CDS 34..1527
XX FT /*tag= a
XX FT /product= "X-linked inhibitor of apoptosis"
XX PN US6087173-A.
XX PD 11-JUL-2000.
XX PF 09-SEP-1999; 99US-0392580.
XX PR 09-SEP-1999; 99US-0392580.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Cowser LM, Ackermann EJ;
XX DR WPI: 2000-498201/44.
XX DR P-PSDB; AAY99985.
XX PT Antisense compound useful for research reagents, diagnostics,
XX PT prophylaxis and for treating disorders associated with X-linked
XX PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
XX PS apoptosis
XX PS Example 13; Column 43-48; 33pp; English.
XX CC The present invention relates to antisense oligonucleotides designed to
XX CC inhibit expression of the human X-linked inhibitor of apoptosis. The
XX CC present sequence is the X-linked inhibitor of apoptosis DNA.
XX CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
XX CC more effective inhibitors than unmodified oligonucleotides. The
XX CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
XX CC expression in cells and tissues in vitro. The oligonucleotides are also
XX CC useful for treating animals or humans, prone to a disease associated
XX CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be
XX CC used prophylactically to prevent infection, inflammation or tumour
XX CC formation.
XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

Query Match 100.08; Score 204; DB 21; Length 2540;
Best Local Similarity 100.08; Pred. No. 1e-57;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
DB 109 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168

QY 61 ACACGTGGCAGCAGCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGGGTGCTTTTACT 120
DB 169 ACACGTGGCAGCAGCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGGGTGCTTTTACT 228

QY 121 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTTGAAGACACAGGAAA 180
DB 229 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTTGAAGACACAGGAAA 288

QY 181 GTATCCCCAAATTCAGATTATC 204
DB 289 GTATCCCCAAATTCAGATTATC 312

RESULT 5
ABK93869
ID ABK93869 standard; cDNA; 2540 BP.
XX: ABK93869;
AC:
XX:
XX:
DT 26-AUG-2002 (first entry)
DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.
OS

```



KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226968-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-CA01379.  
 XX  
 PR 28-SEP-2000; 2000US-0672717.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX  
 DR WPI; 2002-479562/51.  
 DR P-PSDB; ABG65663.  
 XX  
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX  
 PS Disclosure: Fig 1; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
 Query Match 100.0%; Score 204; DB 24; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 1e-57;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGTTTAAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 50  
 DB 109 GAGTTTAAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 168  
 QY 61 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCCTTTAGT 120  
 DB 169 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCCTTTAGT 228  
 QY 121 TGTCTATGACGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGTGGAGACACAGGAAA 180  
 DB 229 TGTCTATGACGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGTGGAGACACAGGAAA 288  
 QY 181 GTATCCCAAAATTCGAGATTATC 204  
 DB 289 GTATCCCAAAATTCGAGATTATC 312

RESULT 6  
 ABK93875  
 ID ABK93875 standard; cDNA; 3000 BP.  
 XX  
 AC ABK93875;  
 XX  
 DT 26-AUG-2002 (first entry)  
 XX  
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
 XX  
 KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226968-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-CA01379.  
 XX  
 PR 28-SEP-2000; 2000US-0672717.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX  
 DR WPI; 2002-479562/51.  
 XX  
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX  
 PS Example 2; Fig 15; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;  
 Query Match 100.0%; Score 204; DB 24; Length 3000;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-57;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGTTTAAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60  
 DB 765 GAGTTTAAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 824  
 QY 61 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCCTTTAGT 120  
 DB 825 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCCTTTAGT 884

QY 121 TGTATGCGAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180  
 DB 885 TGTATGCGAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 944  
 QY 181 GTATCCCAAAATTCAGATTATC 204  
 DB 945 GTATCCCAAAATTCAGATTATC 968  
 RESULT 7  
 AAV55038  
 ID AAV55038 standard; cDNA; 5232 BP.  
 XX AC AAV55038;  
 XX 13-NOV-1998 (first entry)  
 DT  
 DE Human XIAP coding sequence.  
 XX  
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 34..1527  
 FT /\*tag= a  
 FT /product= XIAP  
 FT  
 PN WO9835693-A2.  
 XX  
 XX 20-AUG-1998.  
 XX  
 XX 13-FEB-1998; 98WO-IB00781.  
 XX  
 XX 13-FEB-1997; 97US-0800929.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 XX  
 FI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX  
 XX WPI; 1998-467164/40.  
 DR P-PSDB; AAW69294.  
 XX  
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 XX  
 XX Claim 13; Fig 1; 147pp; English.  
 PS  
 XX This sequence encodes the human XIAP protein, which is an inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis.  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 XX  
 XX Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;  
 SQ  
 Query Match 100.0%; Score 204; DB 19; Length 5232;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-57;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTATAGATTAAAAAATTTTCTGCTAATTTTCCAACTGCTAGTCTCTGTTTCAGCATCA 60  
 DB 109 GAGTTTATAGATTAAAAAATTTTCTGCTAATTTTCCAACTGCTAGTCTCTGTTTCAGCATCA 168  
 QY 61 ACATGCGACAGCAGGAGGTTTCTTTTATCTGTTGAGGAGATACCGTCCGTTGCTTTAGT 120  
 DB 169 ACATGCGACAGCAGGAGGTTTCTTTTATCTGTTGAGGAGATACCGTCCGTTGCTTTAGT 228  
 QY 121 TGTATGCGAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180  
 DB 229 TGTATGCGAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 288  
 QY 181 GTATCCCAAAATTCAGATTATC 204  
 DB 289 GTATCCCAAAATTCAGATTATC 312  
 RESULT 8  
 AAT70839  
 ID AAT70839 standard; cDNA; 2100 BP.  
 XX AC AAT70839;  
 XX 02-SEP-1997 (first entry)  
 DT  
 DE Mouse apoptosis inhibitor m-xiap cDNA.  
 XX  
 KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
 KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
 KW ischaemia; myocardial infarction; stroke;  
 KW reperfusion injury; toxin-induced liver disease; gene therapy;  
 KW diagnosis; ds.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 127..1617  
 FT /\*tag= a  
 FT  
 PN WO9706255-A2.  
 XX  
 XX 20-FEB-1997.  
 XX  
 XX 05-AUG-1996; 96WO-IB01022.  
 XX  
 XX 22-DEC-1995; 95US-0576956.  
 PR 04-AUG-1995; 95US-0511485.  
 XX  
 XX (UYOT-) UNIV OTTAWA.  
 XX  
 XX Baird S, Korneluk RG, Liston P, Mackenzie AE;  
 PI WPI; 1997-154262/14.  
 DR P-PSDB; AAW19584.  
 XX  
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease  
 XX  
 XX Claim 11; Page 78-79; 219pp; English.  
 PS  
 XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and  
 CC hiap-2 genes (AAW70836-41) respectively code for a new class of  
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis  
 CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was  
 CC constructed from 12 overlapping clones isolated from a mouse  
 CC embryo lambda-gt11 cDNA library and from a mouse Fix II genomic  
 CC library using human xiap cDNA as probe. IAP nucleic acids can be  
 CC used to express IAP polypeptides in cells and animals to inhibit  
 CC apoptosis, and as primers and probes to identify and isolate  
 CC additional IAP genes, as well as in methods for treating diseases  
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).

XX SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 84.3%; Score 172; DB 18; Length 2100;  
 Best Local Similarity 90.2%; Pred. No. 4.6e-47;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 60  
 DB 202 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 261

QY 61 ACATGGCAGCAGTGTAGATAGATGGAATATGAGACTGACGCTGGTGGTTCAGT 120  
 DB 322 TGTCTATGAGCAGTGTAGATAGATGGAATATGAGACTGACGCTGGTGGTTCAGT 321

QY 181 GTATCCCAAAATTGCAGATTATC 204  
 DB 382 ATATCCCAAAATTGCAGATTATC 405

RESULT 9  
 ID ABK93872 standard; cDNA; 2100 BP.  
 AC ABK93872;  
 DT 26-AUG-2002 (first entry)  
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.  
 KW Mouse; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX Mus sp.  
 OS  
 PN WO200226968-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-CA01379.  
 XX  
 PR 28-SEP-2000; 2000US-0672717.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX  
 DR WPI: 2002-479562/51.  
 DR P-PSDB; ABG65666.  
 XX  
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX  
 PS Disclosure; Fig 4; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a

CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 84.3%; Score 172; DB 24; Length 2100;  
 Best Local Similarity 90.2%; Pred. No. 4.6e-47;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 60  
 DB 202 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 261

QY 61 ACATGGCAGCAGTGTAGATAGATGGAATATGAGACTGACGCTGGTGGTTCAGT 120  
 DB 262 ACATGGCAGCAGTGTAGATAGATGGAATATGAGACTGACGCTGGTGGTTCAGT 321

QY 121 TGTCTATGAGCAGTGTAGATAGATGGAATATGAGACTGACGCTGGTGGTTCAGT 180  
 DB 322 TGTCTATGAGCAGTGTAGATAGATGGAATATGAGACTGACGCTGGTGGTTCAGT 381

QY 181 GTATCCCAAAATTGCAGATTATC 204  
 DB 382 ATATCCCAAAATTGCAGATTATC 405

RESULT 10  
 ID AAV55041  
 ID AAV55041 standard; cDNA; 2691 BP.  
 XX  
 AC AAV55041;  
 XX  
 DT 13-NOV-1998 (first entry)  
 XX  
 DE Murine XIAP coding sequence.  
 XX  
 DE Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.  
 XX  
 OS Mus sp.  
 FH Key Location/Qualifiers  
 FT CDS 672..2162  
 FT /\*tag= a  
 FT /product= XIAP  
 XX  
 PN WO9835693-A2.  
 XX  
 PD 20-AUG-1998.  
 XX  
 PF 13-FEB-1998; 98WO-IB00781.  
 XX  
 PR 13-FEB-1997; 97US-0800929.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 XX  
 PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX  
 DR WPI: 1998-467164/40.  
 DR P-PSDB; AAW69297.  
 XX  
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving

PT p53 mutations  
XX Claim 13; Fig 4; 147pp; English.  
PS  
CC This sequence encodes the mouse XIAP protein, which is a inhibitor of  
XX apoptosis protein (IAP), and can be used in the method of the invention.  
CC The method is for enhancing apoptosis in cells from a mammal with  
CC proliferative disease by treatment with a compound that inhibits  
CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
CC compounds are used to treat proliferative diseases, specially cancers of  
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
CC rectum, cervix or endometrium, particularly to increase their sensitivity  
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
CC detected in many cancers and are associated with poor prognosis.  
CC resistance to chemotherapeutic agents and mutations in p53 (it is  
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
CC genes). Transgenic animals are used for testing the effects of antisense  
CC oligonucleotides and for screening for the inhibitors.  
XX  
SQ Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;  
Query Match 84.3%; Score 172; DB 19; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 5.1e-47;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCAAGTGGTAGCTGTTTCAGCATCA 50  
Db 747 GAGTTTAATAGATTAAACATTTTCTTAATTTTCAAGTGGTAGCTGTTTCAGCATCA 806  
Qy 61 ACATGGCAGCAGCAGGCTTCTTTATACCTGCTGAAGGAGATACCGTGGTGTCTTAGT 120  
Db 807 ACATGGCAGCAGCAGGCTTCTTTATACCTGCTGAAGGAGATACCGTGGTGTCTTAGT 866  
Qy 121 TGTCATGAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 180  
Db 867 TGTCATGCGGCAATAGATAGATGGCAATATGGAGACTCAGCAGTGGAGACACAGGAGA 926  
Qy 181 GTATCCCCAAATTCAGATTATC 204  
Db 927 ATATCCCCAAATTCAGATTATC 950  
RESULT 11  
AA72710  
ID AA72710 standard; DNA; 1988 BP.  
XX  
XX AA72710;  
XX  
XX 16-SEP-1997 (first entry)  
XX  
XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.  
XX  
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;  
KW degenerative disease; infectious disease; autoimmune disease;  
KW cancer; gene therapy; diagnosis; ss.  
XX  
XX Mus musculus.  
XX  
XX Key Location/Qualifiers  
XX CDS 212..1702  
XX /\*tag- a  
XX  
XX WO9723501-A1.  
XX  
XX 03-JUL-1997.  
XX  
XX 20-DEC-1996; 96WO-AU00827.  
XX  
XX 22-DEC-1995; 95AU-0007275.  
XX  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX

PI Vaux DL;  
XX  
XX WPI: 1997-350966/32.  
DR P-PSDB; AA719745.  
XX  
XX Isolated protein homologues of viral inhibitors of apoptosis - used  
PT to modulate apoptosis for treatment of degenerative, infectious or  
PT autoimmune diseases and cancer  
XX  
XX Claim 24; Page 44-47; 136pp; English.  
PS  
XX An isolated nucleic acid molecule (AA72710) codes for mammalian IAP  
CC homologue A (MIHA) (AA719745), a murine homologue of baculovirus  
CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse  
CC liver cDNA library on the basis of homology to Orgyia pseudotsuguta  
CC polyhedrosis virus IAP BIR and RING finger amino acid motifs.  
CC Animal IAP homologue nucleic acids (see also AA72711-17) can be used  
CC to produce polypeptides useful in methods for modulating apoptosis  
CC in animal cells, specifically for treatment, by inhibition, of  
CC degenerative and infectious disease or, by promotion, of cancer and  
CC autoimmune disease, and can be used for gene therapy of these  
CC diseases.  
XX  
SQ Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;  
Query Match 83.5%; Score 170.4; DB 18; Length 1988;  
Best Local Similarity 89.7%; Pred. No. 1.5e-46;  
Matches 183; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCAAGTGGTAGCTGTTTCAGCATCA 60  
Db 287 GAGTTTAATAGATTAAACATTTTCTTAATTTTCAAGTGGTAGCTGTTTCAGCATCA 346  
Qy 61 ACATGGCAGCAGCAGGCTTCTTTATACCTGCTGAAGGAGATACCGTGGTGTCTTAGT 120  
Db 347 ACATGGCAGCAGCAGGCTTCTTTATACCTGCTGAAGGAGATACCGTGGTGTCTTAGT 406  
Qy 121 TGTCATGAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 180  
Db 407 TGTCATGCGGCAATAGATAGATGGCAATATGGAGACTCAGCAGTGGAGACACAGGAGA 466  
Qy 181 GTATCCCCAAATTCAGATTATC 204  
Db 467 ATATCCCCAAATTCAGATTATC 490  
RESULT 12  
ABL54307  
ID ABL54307 standard; DNA; 7990 BP.  
XX  
XX ABL54307;  
XX  
XX 29-JUL-2002 (first entry)  
XX  
XX Chemically treated apoptosis gene #4.  
XX  
XX Apoptosis; HIV; Bloom syndrome; cardiopathy;  
KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;  
KW amyotrophic lateral sclerosis; cancer; ds.  
XX  
XX Unidentified.  
XX  
XX WO200177164-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-EP03969.  
XX  
XX 06-APR-2000; 2000DE-1019058.  
XX  
XX 07-APR-2000; 2000DE-1019173.  
XX  
XX 30-JUN-2000; 2000DE-1032529.  
XX  
XX 01-SEP-2000; 2000DE-1043826.  
XX

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PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-017444/02.
XX Chemically modified sequences of genes associated with apoptosis are
XX useful to determine methylation patterns of genomic DNA samples for
XX diagnosis of associated diseases such as cancer
XX
XX Claim 1; Seq ID #7; 24pp; English.
XX This invention relates to chemically pre-treated DNA of genes
XX associated with apoptosis. The nucleic acids are used to allocate
XX patients for specific therapy for HIV infection, Bloom syndrome, virus
XX cardiopathy, aging, neurodegenerative disorders, Herpes simplex, virus
XX infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours
XX and cancers. This nucleotide sequence represents a chemically
XX treated apoptosis gene. Even SEQ ID numbers are the complementary
XX DNA strands to the odd SEQ ID numbers. The sequence data for this
XX patent is not represented in the printed specification but is based on
XX information supplied by the European patent office.
XX
XX Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;
XX
Query Match 75.2%; Score 153.4; DB 24; Length 7990;
Best Local Similarity 84.7%; Pred. No. 1.4e-40;
Matches 172; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 GAGTTAATAGATTAAACCTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
Db 5109 GAGTTAATAGATTAAACCTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
QY 61 ACACCTGGCAGCAGCGGTTCTTTTATCTGCTGAAGCAGATACCGTGGCTTTTACT 120
Db 5169 ATATTGGTACGAGTAGGGTTTTTTTATATTGTTGAAGGAGATATCGTGGGTTTACT 528
QY 121 TGTCATGACGCTGTAGATAGATGGAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180
Db 5229 TGTTATGATGTTGTAGATAGATGGAATATGAGACTCAGCAGTTGGAGATATAGGAAA 5288
QY 181 GTATCCCAAAATGCGAGATTAT 203
Db 5289 GTATTTTAAATGTTAGATTAT 5311
RESULT 13
ABL32158
ID ABL32158 standard; DNA; 7990 BP.
XX ABL32158;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human immune system associated gene SEQ ID NO: 131.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antianaemic; cytosolic; neutropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation
XX
XX Claim 1; SEQ ID NO 131; 32pp + Sequence Listing; German.
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.
XX
XX Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;
XX
Query Match 75.2%; Score 153.4; DB 24; Length 7990;
Best Local Similarity 84.7%; Pred. No. 1.4e-40;
Matches 172; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 GAGTTAATAGATTAAACCTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
Db 5109 GAGTTAATAGATTAAACCTTTCTTAATTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
QY 61 ACACCTGGCAGCAGCGGTTCTTTTATCTGCTGAAGCAGATACCGTGGCTTTTACT 120
Db 5169 ATATTGGTACGAGTAGGGTTTTTTTATATTGTTGAAGGAGATATCGTGGGTTTACT 528
QY 121 TGTCATGACGCTGTAGATAGATGGAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180
Db 5229 TGTTATGATGTTGTAGATAGATGGAATATGAGACTCAGCAGTTGGAGATATAGGAAA 5288
QY 181 GTATCCCAAAATGCGAGATTAT 203
Db 5289 GTATTTTAAATGTTAGATTAT 5311
RESULT 14
ABL54308/C
ID ABL54308 standard; DNA; 7990 BP.
XX ABL54308;
XX
XX 29-JUL-2002 (first entry)
XX
XX Chemically treated apoptosis gene complementary to gene #4.
XX
XX Apoptosis; HIV; Bloom syndrome; cardiopathy;
XX neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
XX amyotrophic lateral sclerosis; cancer; ds.
XX
XX Unidentified.
XX
XX WO200177164-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-EP03969.
XX
XX 06-APR-2000; 2000DE-1019058.
XX 07-APR-2000; 2000DE-1019173.
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.

```

XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX XX WPI; 2002-017444/02.  
 XX DR Chemically modified sequences of genes associated with apoptosis are  
 XX PT useful to determine methylation patterns of genomic DNA samples for  
 XX PT diagnosis of associated diseases such as cancer -  
 XX PS Claim 1; Seq ID #8; 24pp; English.  
 XX CC This invention relates to chemically pre-treated DNA of genes  
 XX CC associated with apoptosis. The nucleic acids are used to allocate  
 XX CC patients for specific therapy for HIV infection, Bloom syndrome,  
 XX CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus  
 XX CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours  
 XX CC and cancers. This nucleotide sequence represents a chemically  
 XX CC treated apoptosis gene. Even SEQ ID numbers are the complementary  
 XX CC DNA strands to the odd SEQ ID numbers. The sequence data for this  
 XX CC patent is not represented in the printed specification but is based on  
 XX CC information supplied by the European patent office.  
 XX SQ Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;

Query Match 63.4%; Score 129.4; DB 24; Length 7990;  
 Best Local Similarity 77.3%; Pred. No. 1.4e-32;  
 Matches 157; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 2 AGTTTATAGATTAAAAAAGCTTTTCTTAATTTTCCAAAGTGGTAGCTCTGTTTCAGCATCAA 61  
 DB 2881 AATTATAAATTAATAAAGCTTTTCTTAATTTTCCAAATATAATCTTATTTCAACATCAA 2822

QY 62 CACTGGCAGCAGCAGGGTTTCTTATCTACTGTTGAAGGAGATACCGTGGGCTTTAGTT 121  
 DB 2821 CACTAACACGACAAATTTCTTTATCTACTATAAAAAAATACCGTACGATACTTAAT 2762

QY 122 GTCATGAGCTGTAGATAGATGGCAATATGGAGACTACGAGTGGGAGACACAGGAAG 181  
 DB 2761 ATCATCAACTATATAATAAATAACAATATAAAAACTCAACAATTAATAAAACACAAAAA 2702

QY 182 TATCCCAAAATTCAGATTTATC 204  
 DB 2701 TATCCCAAAATTCAGATTTATC 2679

## RESULT 15

ABL32159/c  
 ID ABL32159 standard; DNA; 7990 BP.

XX AC ABL32159;

XX AC ABL32159;

XX DT 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 132.

XX KW Human; immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; anti-amyloid; cytosine methylation; antiasthmatic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antirheumatic; antiarthritic; antidiabetic; antiporiatic;  
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.

XX OS Homo sapiens.

XX PN WO200200928-A2.

XX PD 03-JAN-2002.

XX PF 02-JUL-2001; 2001WO-EP07537.

XX

30-JUN-2000; 2000DE-1032529.  
 01-SEP-2000; 2000DE-1043826.

(EPIC-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2002-130909/17.

Nucleic acid comprising fragment of chemically modified gene, useful  
 for diagnosis and treatment of diseases associated with abnormal  
 cytosine methylation -

Claim 1; SEQ ID NO 132; 32pp + Sequence Listing; German.

The present invention provides a number of human immune system associated  
 genes which are modified by the methylation of cytosines. The sequences  
 can be used in the diagnosis and treatment of immune system disorders,  
 including eye diseases such as retinopathy, neovascular glaucoma and  
 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 diseases. The present sequence is a gene of the invention.

Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;

Query Match 63.4%; Score 129.4; DB 24; Length 7990;  
 Best Local Similarity 77.3%; Pred. No. 1.4e-32;  
 Matches 157; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 2 AGTTTATAGATTAAAAAAGCTTTTCTTAATTTTCCAAAGTGGTAGCTCTGTTTCAGCATCAA 61

DB 2881 AATTATAAATTAATAAAGCTTTTCTTAATTTTCCAAATATAATCTTATTTCAACATCAA 2822

QY 62 CACTGGCAGCAGCAGGGTTTCTTATCTACTGTTGAAGGAGATACCGTGGGCTTTAGTT 121

DB 2821 CACTAACACGACAAATTTCTTTATCTACTATAAAAAAATACCGTACGATACTTAAT 2762

QY 122 GTCATGAGCTGTAGATAGATGGCAATATGGAGACTACGAGTGGGAGACACAGGAAG 181

DB 2761 ATCATCAACTATAATAAATAACAATATAAAAACTCAACAATTAATAAAACACAAAAA 2702

QY 182 TATCCCAAAATTCAGATTTATC 204

DB 2701 TATCCCAAAATTCAGATTTATC 2679

## RESULT 15

ABL32159/c  
 ID ABL32159 standard; DNA; 7990 BP.

XX AC ABL32159;

XX AC ABL32159;

XX DT 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 132.

XX KW Human; immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; anti-amyloid; cytosine methylation; antiasthmatic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antirheumatic; antiarthritic; antidiabetic; antiporiatic;  
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.

XX OS Homo sapiens.

XX PN WO200200928-A2.

XX PD 03-JAN-2002.

XX PF 02-JUL-2001; 2001WO-EP07537.

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 25.6771 Seconds

(without alignments)

2436.494 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gagtttaataagattaaac.....ccccaaattgcagatttattc 204

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	204	100.0	1588	4	US-09-239-867-3
2	204	100.0	2540	2	US-08-511-485-3
3	204	100.0	2540	3	US-09-392-580-1
4	204	100.0	5232	3	US-09-212-971-3
5	204	100.0	5232	3	US-08-800-929A-3
6	204	100.0	5232	4	US-09-617-053A-3
7	172	84.3	2100	2	US-08-511-485-9
8	172	84.3	2691	3	US-09-212-971-9
9	172	84.3	2691	3	US-08-800-929A-9
10	172	84.3	2691	4	US-09-617-053A-9
11	68.4	33.5	1559	4	US-09-239-867-1
12	62.2	30.5	2676	3	US-09-212-971-11
13	62.2	30.5	2676	3	US-08-800-929A-11
14	62.2	30.5	2676	4	US-09-617-053A-11
15	62.2	30.5	2862	4	US-08-569-749-13
16	62.2	30.5	2862	5	PCT-US96-12860-13
17	62.2	30.5	3151	3	US-09-212-971-13
18	62.2	30.5	3151	3	US-08-800-929A-13
19	62.2	30.5	3151	4	US-09-617-053A-13
20	56	27.5	3076	2	US-08-511-485-5
21	56	27.5	3076	2	US-09-205-144-1
22	56	27.5	6669	3	US-09-212-971-5
23	56	27.5	6669	3	US-08-800-929A-5
24	56	27.5	6669	4	US-09-617-053A-5
25	55.8	27.4	2580	2	US-08-511-485-7
26	55.8	27.4	2589	4	US-08-569-749-1
27	55.8	27.4	2589	5	PCT-US96-12860-1

28 55.8 27.4 3532 2 US-09-205-204-1 Sequence 1, Appli  
29 55.8 27.4 3732 3 US-09-212-971-7 Sequence 7, Appli  
30 55.8 27.4 3732 3 US-08-800-929A-7 Sequence 7, Appli  
31 55.8 27.4 3732 4 US-09-617-053A-7 Sequence 7, Appli  
32 54.4 26.7 2601 4 US-08-569-749-3 Sequence 3, Appli  
33 54.4 26.7 2601 5 PCT-US96-12860-3 Sequence 3, Appli  
34 52.2 25.6 5502 3 US-08-836-134-1 Sequence 1, Appli  
35 52.2 25.6 5502 4 US-09-493-784-1 Sequence 1, Appli  
36 42.4 20.8 1435 5 PCT-US95-05922A-1 Sequence 1, Appli  
37 34.4 16.9 711 3 US-09-121-979-3 Sequence 3, Appli  
38 34.4 16.9 711 4 US-09-322-319-3 Sequence 3, Appli  
39 31.4 15.4 374 4 US-09-328-111-423 Sequence 423, App  
40 30.8 15.1 176373 3 US-09-128-155-17 Sequence 17, Appli  
41 30.4 14.9 1725 4 US-09-062-440-1 Sequence 1, Appli  
42 30.4 14.9 1725 4 US-09-712-495-1 Sequence 1, Appli  
43 29 14.2 2556 3 US-08-699-103B-9 Sequence 9, Appli  
44 29 14.2 2556 4 US-09-229-059-9 Sequence 9, Appli  
45 29 14.2 2731 3 US-08-699-103B-11 Sequence 11, Appli

#### ALIGNMENTS

RESULT 1  
US-09-239-867-3  
; Sequence 3, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-239-867-3

Query Match 100.0% Score 204; DB 4; Length 1588;  
Best Local Similarity 100.0%; Pred. No. 1,le-55;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60  
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Db 109 GAGTTTAATAGATTAAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168  
QY 61 ACACGTGGCAGCAGCAGGGTTCTTTTATCTGTGAAGGAGATACCGTGGGTGCTTTAGT 120  
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Db 169 ACACGTGGCAGCAGCAGGGTTCTTTTATCTGTGAAGGAGATACCGTGGGTGCTTTAGT 228  
QY 121 TGTCTATGACGCTAGATAGATGAGCAATATGAGACTCAGCAGTGTGGAAGACACAGCAAA 180  
|||||  
Db 229 TGTCTATGACGCTAGATAGATGAGCAATATGAGACTCAGCAGTGTGGAAGACACAGCAAA 288  
QY 181 GTATCCCAAAATTCAGATTATTC 204  
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Db 289 GTATCCCAAAATTCAGATTATTC 312  
RESULT 2  
US-08-511-485-3  
; Sequence 3, Application US/08511485  
; Patent No. 5919912  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2540 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-511-485-3

Query Match 100.0%; Score 204; DB 2; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 1.4e-55;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 60  
|||||  
DB 109 GAGTTTAATAGATTAAACACTTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 168  
QY 61 ACACCTGGCAGCAGCAGGGTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 120  
|||||  
DB 169 ACACCTGGCAGCAGCAGGGTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 228  
QY 121 TGTCTATGACCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAA 180  
|||||  
DB 229 TGTCTATGACCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAA 288  
QY 181 GTATCCCAAAATTCAGATTATC 204  
|||||  
DB 289 GTATCCCAAAATTCAGATTATC 312

## RESULT 3

US-09-392-580-1  
Sequence 1, Application US/09392580  
Patent No. 6087173  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
APPLICANT: Lex M. Cowser  
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION  
FILE REFERENCE: R1S-0072  
CURRENT APPLICATION NUMBER: US/09/392,580  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 1  
LENGTH: 2540  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (34)...(1527)  
US-09-392-580-1

Query Match 100.0%; Score 204; DB 3; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 1.4e-55;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 60  
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DB 109 GAGTTTAATAGATTAAACACTTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 168  
QY 61 ACACCTGGCAGCAGCAGGGTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 120  
|||||  
DB 169 ACACCTGGCAGCAGCAGGGTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 228  
QY 121 TGTCTATGACCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAA 180  
|||||  
DB 229 TGTCTATGACCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAA 288  
QY 181 GTATCCCAAAATTCAGATTATC 204  
|||||  
DB 289 GTATCCCAAAATTCAGATTATC 312

## RESULT 4

US-09-212-971-3  
Sequence 3, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5232  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4623)...(4623)  
OTHER INFORMATION: n can be any nucleotide  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4622)...(4622)  
OTHER INFORMATION: n can be any nucleotide  
US-09-212-971-3

Query Match 100.0%; Score 204; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 1.8e-55;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 60  
|||||  
DB 109 GAGTTTAATAGATTAAACACTTTTCTTATCTGTTTCCAAAGTGGTAGTCCTCTTTTCAGCATCA 168



Qy	181	GTATCCCAAAATTGCAGATTTATC	204
Dβ	289	GTATCCCAAAATTGCAGATTTATC	312

```

: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009003
: CURRENT APPLICATION NUMBER: US/09/617,053A
: CURRENT FILING DATE: 2000-07-14
: PRIOR FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 5232
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: variation
: LOCATION: (4623)...(4623)
: OTHER INFORMATION: n can be any nucleotide
: NAME/KEY: variation
: LOCATION: (4622)...(4622)
: OTHER INFORMATION: n can be any nucleotide
:
: US-09-617-053A-3

Query Match      100.08; Score 204; DB 4; Length 5232;
Best Local Similarity 100.08; Pred. No. 1.8e-55;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1  GAGTTTAATAGATTAATAAACTTTTGCCTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
      |||
Db      109 GAGTTTAATAGATTAATAAACTTTTGCCTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 168

Qy      61  ACACATGGCACGACGAGGGTTTCTTTTACTGGTGAAGGAGATACCGTGGCGTGCTTTAGT 120
      |||
Db      169 ACACATGGCACGACGAGGGTTTCTTTTACTGGTGAAGGAGATACCGTGGCGTGCTTTAGT 228

Qy      121 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACACAGAAA 180
      |||
Db      229 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACACAGAAA 288

Qy      181 GTATCCCAAAATTCAGATTATC 204
      |||
Db      289 GTATCCCAAAATTCAGATTATC 312

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```
RESULT 7
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 591912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511.485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match      84.3%  Score 172; DB 2; Length 2100;
Best Local Similarity 90.2%  Pred. No. 1.9e-45;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCCAAGTGGTAGTCCTGTTTCAGCATCA 60
|||||
DB 202 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCCAAGTGGTAGTCCTGTTTCAGCATCA 261
|||||

QY 61 ACACGTGGCAGCAGAGGGTTCCTTTATCTGTTGAAGAGATACCGTGGCGGCTTTTACT 120
|||||
DB 262 ACATTTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 321
|||||

QY 121 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
|||||
DB 322 TGTCTATGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTTGAAGACACAGGAGA 381
|||||

QY 181 GPATCCCCAAATTGCAGATTATC 204
|||||
DB 382 ATATCCCCAAATTGCAGATTATC 405
|||||

RESULT 8
US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212.971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

Query Match      84.3%  Score 172; DB 3; Length 2691;
Best Local Similarity 90.2%  Pred. No. 2.1e-45;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCCAAGTGGTAGTCCTGTTTCAGCATCA 60
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DB 747 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCCAAGTGGTAGTCCTGTTTCAGCATCA 806
|||||

QY 61 ACACGTGGCAGCAGCAGGGTTCCTTTATCTGTTGAAGAGATACCGTGGCGGCTTTTACT 120
|||||
DB 807 ACATTTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTTCAGT 866
|||||

QY 121 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
|||||
DB 867 TGTCTATGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTTGAAGACACAGGAGA 926
|||||

QY 181 GPATCCCCAAATTGCAGATTATC 204
|||||
DB 927 ATATCCCCAAATTGCAGATTATC 950
|||||

RESULT 9
US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/800,929A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,590  
; FILING DATE: 14-NOV-1996  
; APPLICATION NUMBER: 60/017,354  
; FILING DATE: 26-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bleker-Brady, Kristina  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 07891/009001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2691 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-800-929A-9

Query Match 84.3%; Score 172; DB 3; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 2.le-45;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
  
QY 1 GAGTTTAAATAGATTAAAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 60  
DB 747 GAGTTTAAATAGATTAAAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 806  
  
QY 61 ACATGGCAGCAGCAGGCTTTCTTTATACCTGTTGAAGGAGATACCGTGGTGTCTTTAGT 120  
DB 807 ACATTGGCGGAGCTGGGTTCTTTATACCGTGTGAAGGAGACACCGTGCATGTTTCAGT 866  
  
QY 121 TGTATCGCAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 180  
DB 867 TGTATCGGCGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTTGAAGACACAGGAGA 926  
  
QY 181 GTATCCCCAAATTCAGATTATC 204  
DB 927 ATATCCCCAAATTCAGATTATC 950

RESULT 10  
US-09-617-053A-9  
; Sequence 9, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009003  
; CURRENT APPLICATION NUMBER: US/09/617,053A  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2691  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-617-053A-9

Query Match 84.3%; Score 172; DB 4; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 2.le-45;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
  
QY 1 GAGTTTAAATAGATTAAAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 60  
DB 747 GAGTTTAAATAGATTAAAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 806  
  
QY 61 ACATGGCAGCAGCAGGCTTTCTTTATACCTGTTGAAGGAGATACCGTGGTGTCTTTAGT 120  
DB 807 ACATTGGCGGAGCTGGGTTCTTTATACCGTGTGAAGGAGACACCGTGCATGTTTCAGT 866  
  
QY 121 TGTATCGCAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 180  
DB 867 TGTATCGGCGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTTGAAGACACAGGAGA 926  
  
QY 181 GTATCCCCAAATTCAGATTATC 204  
DB 927 ATATCCCCAAATTCAGATTATC 950

RESULT 11  
US-09-239-867-1  
; Sequence 1, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; TITLE OF INVENTION: MALE FERTILITY  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1559  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)-(1559)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-239-867-1

Query Match 33.5%; Score 68.4; DB 4; Length 1559;  
Best Local Similarity 64.7%; Pred. No. 1.6e-12;  
Matches 132; Conservative 0; Mismatches 46; Indels 26; Gaps 1;  
  
QY 1 GAGTTTAAATAGATTAAAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 60  
DB 109 GAGATTAAATAGATCAAAAACGTTTGTGCTTTGAGGTGGTGGCTGCTGGGCGCATCG 168  
  
QY 61 ACATGGCAGCAGCAGGCTTTCTTTATACCTGTTGAAGGAGATACCGTGGTGTCTTTAGT 120  
DB 169 GGC-----GTTGAGGAGAGACGCCCTGGGGGGGCTTACG 202  
  
QY 121 TGTATCGCAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 180  
DB 203 TCCCTGAGCGGTAGACAGGTGGCAACCTGGGGCTCAGGAGTTGACAAACACACAGAAA 262  
  
QY 181 GTATCCCCAAATTCAGATTATC 204  
DB 263 GCAGGCGCGAATTCAGATTATC 286

RESULT 12  
US-09-212-971-11  
; Sequence 11, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 2676  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-212-971-11

Query Match 30.5%; Score 62.2; DB 3; Length 2676;  
Best Local Similarity 56.7%; Pred. No. 1.8e-10;  
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 1 GAGTTTATAGATTAATAAACTTTCTCTAATTTTCCAACTGGTAGTCTCTGTTTCAGCATCA 60  
DB 381 GAGCTGTACCGATTTCCACGATTCACGTTTCCAGGGAGTCTCTGTGCAGAAAGG 440  
QY 61 ACACCTGGCAGCAGGAGGTTTCTTTTACTGTGTGAAGGAGATACCGTGGGTGCTTTAGT 120  
DB 441 AGTCTGGCTGCTGTGGCTTTTACTACACTGTGTGCAATGACAAAGGTCAAGTCTCTGC 500  
QY 121 TGTATGACGCTGTAGTAGATGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180  
DB 501 TGTGSCCTGTAGTACAACTGGAACAGGGGACATCCCATGAGAGACACAGAAAG 560  
QY 181 GTATCCCAAAATTCAGATTAT 203  
DB 561 TTGTACCCCGAGTGCACACTTTGT 583

RESULT 13  
US-08-800-929A-11  
Sequence 11, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2676 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-800-929A-11

Query Match 30.5%; Score 62.2; DB 3; Length 2676;  
Best Local Similarity 56.7%; Pred. No. 1.8e-10;  
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 1 GAGTTTATAGATTAATAAACTTTCTCTAATTTTCCAACTGGTAGTCTCTGTTTCAGCATCA 60  
DB 381 GAGCTGTACCGATTTCCACGATTCACGTTTCCAGGGAGTCTCTGTGCAGAAAGG 440  
QY 61 ACACCTGGCAGCAGGAGGTTTCTTTTACTGTGTGAAGGAGATACCGTGGGTGCTTTAGT 120  
DB 441 AGTCTGGCTGCTGTGGCTTTTACTACACTGTGTGCAATGACAAAGGTCAAGTCTCTGC 500  
QY 121 TGTATGACGCTGTAGTAGATGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180  
DB 501 TGTGSCCTGTAGTACAACTGGAACAGGGGACATCCCATGAGAGACACAGAAAG 560  
QY 181 GTATCCCAAAATTCAGATTAT 203  
DB 561 TTGTACCCCGAGTGCACACTTTGT 583

RESULT 14  
US-09-617-053A-11  
Sequence 11, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US/08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 2676  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-617-053A-11

Search completed: April 16, 2003, 00:57:28  
Job time : 29.6771 secs

RESULT 15  
US-08-569-749-13

Query Match	30.5%	Score 62.2;	DB 4;	Length 2862;
Best Local Similarity	56.7%;	Pred. No. 1.e-10;		
Matches 115;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps

  

QY	1	GAGTTTAAATAGATAAAAACTTTTGCTAATTTCGAAGTGGTAGTCTCTTTCCAGCATCA	60
Db	608	GAACCTCACCGAATGCTCAGATATTACGCTTTTCCCAGGGAGTTCCTGTCTCAGAGAGG	667
QY	61	ACACTGSCAGCAGCAGGGTTCTTTATCTGGTGAAGAGATACCCTGCCTGCTTTTACT	120

Query Match 30.5%; Score 62.2; DB 4; Length 2862;  
Best Local Similarity 56.7%; Pred. NO. 1.8e-10;  
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 49.0521 Seconds  
(without alignments)  
3648.005 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gaggtttaaatagattaaac.....ccccaaattgcagattatc 204

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186658

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/2/pubpna/PC1\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PC1US\_PUBCOMB.seq.\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	204	100.0	2540	9	US-09-201-936-3
3	204	100.0	5232	10	US-09-974-592-3
4	172	84.3	2100	9	US-09-201-936-9
5	172	84.3	2691	10	US-09-974-592-9
6	62.2	30.5	2416	9	US-09-201-936-41
7	62.2	30.5	2450	9	US-09-201-936-39
8	62.2	30.5	2676	10	US-09-974-592-11
9	62.2	30.5	3151	10	US-09-974-592-13
10	56	27.5	2676	9	US-09-201-936-5
11	56	27.5	3076	9	US-09-954-531-16
12	56	27.5	3076	10	US-09-954-456-1635
13	56	27.5	6669	10	US-09-974-592-5
14	55.8	27.4	2580	9	US-09-201-936-7
15	55.8	27.4	3532	10	US-09-880-107-3354
16	55.8	27.4	3732	10	US-09-974-592-7
17	54.2	26.6	2291	10	US-09-778-927A-21
18	52.2	25.6	5504	8	US-08-913-322-1
19	52.2	25.6	6124	8	US-08-913-322-21

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Sequence 2, Appli  
Sequence 23, Appli  
Sequence 6687, Ap  
Sequence 3493, Ap  
Sequence 3213, Ap  
Sequence 182, App  
Sequence 182, App  
Sequence 423, App  
Sequence 248, App  
Sequence 17, Appli  
Sequence 140, App  
Sequence 51, Appli  
Sequence 1598, Ap  
Sequence 1, Appli  
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Sequence 125, App  
Sequence 116, App  
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20 52.2 25.6 6124 10 US-09-967-768A-184  
21 52.2 25.6 6133 8 US-08-913-322-2  
22 52.2 25.6 6228 8 US-08-913-322-23  
23 41 20.1 240 9 US-09-796-692-5687  
24 39.4 19.3 240 9 US-09-796-692-3493  
25 31.4 15.4 285 9 US-09-796-692-3213  
26 31.4 15.4 314 10 US-09-920-300A-182  
27 31.4 15.4 314 12 US-10-033-528-182  
28 31.4 15.4 374 10 US-09-879-536-423  
29 31.4 15.4 571 12 US-10-044-090-248  
30 30.8 15.1 176373 9 US-10-095-407-17  
31 30.6 15.0 7992 9 US-08-893-519A-140  
32 30.6 15.0 8493 9 US-10-071-766-51  
33 30.4 14.9 1587 9 US-09-938-842A-1598  
34 30.4 14.9 1725 9 US-10-075-074-1  
35 29.8 14.6 11186 10 US-09-957-997-1  
36 29.6 14.5 2193 10 US-09-801-368-125  
37 29.6 14.5 2851 9 US-10-114-893-116  
38 29.6 14.5 2906 9 US-09-905-291A-291  
39 29.6 14.5 2906 9 US-09-992-598-500  
40 29.6 14.5 2906 9 US-09-989-293A-500  
41 29.6 14.5 2906 9 US-09-902-853-291  
42 29.6 14.5 2906 9 US-09-989-735-500  
43 29.6 14.5 2906 9 US-09-990-444-500  
44 29.6 14.5 2906 9 US-09-907-824-291  
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#### ALIGNMENTS

RESULT 1  
US-09-964-899-38  
; Sequence 38, Application US/09964899  
; Patent NO. US20020174446A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Dalia et al.  
; TITLE OF INVENTION: Identification of Genes Involved in  
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster  
; FILE REFERENCE: 4-31612 A  
; CURRENT APPLICATION NUMBER: US/09/964,899  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 60/236,893  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/298,309  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; US-09-964-899-38

Query Match 100.0%; Score 204; DB 9; Length 2404;  
Best Local Similarity 100.0%; Pred. No. 2.5e-56;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGTTTAAATAGATTAAACCTTTTCTAATTTTCCAAGTGGTAGTCCTCTTTTCAGCATCA 60  
|||||  
Db 109 GAGTTTAAATAGATTAAACCTTTTCTAATTTTCCAAGTGGTAGTCCTCTTTTCAGCATCA 168  
Qy 61 ACACCTGGCAGCAGCAGGGTTCCTTTTACTGTGTGAAGAGATACCGTGGCGGTCTTTTACT 120  
|||||  
Db 169 ACACCTGGCAGCAGCAGGGTTCCTTTTACTGTGTGAAGAGATACCGTGGCGGTCTTTTACT 228  
Qy 121 TGTCTAATGAGCTGTAGATAGATGGCAATATGAGACTCAGACTGAGAGACACAGGAAA 180  
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Db 229 TGTCTAATGAGCTGTAGATAGATGGCAATATGAGACTCAGACTGAGAGACACAGGAAA 288  
Qy 181 GTATCCCAAAATTCGAGATTATTC 204  
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Db 289 GTATCCCAAAATTCGAGATTATTC 312



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Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAATAAATCTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
Db 202 GAGTTTAATAGATTAATAAATCTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 261
QY 61 ACACCTGGCAGCAGCGGGTCTTTATACCTGGTGAAGGAGATACCGTGGTGGTCTTTAGT 120
Db 262 ACATTTGGCGGAGCTGGGGTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 321
QY 121 TGTCTATGCACGCTGTAGATAGTGGCAATATGGAGACTCAGCAGTGTGGAAAGACACAGGAAA 180
Db 322 TGTCTATGCACGCTGTAGATAGTGGCAATATGGAGACTCAGCAGTGTGGAAAGACACAGGAGA 381
QY 181 GTATCCCAAAATTCAGATTATC 204
Db 382 ATATCCCAAAATTCAGATTATC 405
RESULT 5
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; FILE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9
Query Match 84.3%; Score 172; DB 10; Length 2691;
Best Local Similarity 90.2%; Pred. No. 7e-46;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAATAAATCTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
Db 747 GAGTTTAATAGATTAATAAATCTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 806
QY 61 ACACCTGGCAGCAGCGGGTCTTTATACCTGGTGAAGGAGATACCGTGGTGGTCTTTAGT 120
Db 807 ACATTTGGCGGAGCTGGGGTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 866
QY 121 TGTCTATGCACGCTGTAGATAGTGGCAATATGGAGACTCAGCAGTGTGGAAAGACACAGGAAA 180
Db 867 TGTCTATGCACGCTGTAGATAGTGGCAATATGGAGACTCAGCAGTGTGGAAAGACACAGGAGA 926
QY 181 GTATCCCAAAATTCAGATTATC 204
Db 927 ATATCCCAAAATTCAGATTATC 950
RESULT 6
US-09-201-936-41
; Sequence 41, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-08-04
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2450
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; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-08-04
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-41
Query Match 30.5%; Score 62.2; DB 9; Length 2416;
Best Local Similarity 56.7%; Pred. No. 3.8e-10;
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAATAAATCTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
Db 215 GAGTTTAATAGATTAATAAATCTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 274
QY 61 ACACCTGGCAGCAGCGGGTCTTTATACCTGGTGAAGGAGATACCGTGGTGGTCTTTAGT 120
Db 275 AGTCTGGCTGCTGCTGGCTTTTATATACAGGTGTGAATGACAAAGTCAAGTGTCTCTGC 334
QY 121 TGTCTATGCACGCTGTAGATAGTGGCAATATGGAGACTCAGCAGTGTGGAAAGACACAGGAAA 180
Db 335 TGTCTATGCACGCTGTAGATAGTGGCAATATGGAGACTCAGCAGTGTGGAAAGACACAGGAAA 394
QY 181 GTATCCCAAAATTCAGATTATC 203
Db 395 TTCTATCCCAAGCTGCAGCTTGT 417
RESULT 7
US-09-201-936-39
; Sequence 39, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-08-04
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2450
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EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 2676  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (2470)...(2470)  
OTHER INFORMATION: N may be any nucleotide  
FEATURE:  
NAME/KEY: variation  
LOCATION: (2476)...(2476)  
OTHER INFORMATION: N may be any nucleotide  
FEATURE:  
NAME/KEY: variation  
LOCATION: (2483)...(2483)  
OTHER INFORMATION: N may be any nucleotide  
FEATURE:  
NAME/KEY: variation  
LOCATION: (2602)...(2602)  
OTHER INFORMATION: N may be any nucleotide  
US-09-201-936-5

Query Match 27.5%; Score 56; DB 9; Length 2676;  
Best Local Similarity 55.0%; Pred. No. 4.2e-08;  
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACACTTTTGCTAATTTTCCAACTGGTAGTCCTGTTTTCAGCATCA 60  
Db 273 GAACGTGTACCGAATGCTCTACGTATTCACACTTTTCTGCTGGGTTCCCTGCTCAGAAAGG 332  
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGGTGAAGAGATACCGTCCGGTGGCTTTAGT 120  
Db 333 AGTCTTGCTGCTGGTGTCTTATACACTGGTGTGAATGACAGGTCAAATGCTTCTGT 392  
Qy 121 TGTCTATGACGTGTAGATAGATGGAATATGGAGACTCAGCAGTGTGGAAGACACAGGAAA 180  
Db 393 TGTGCTCTGATGCTGGATACTGGAAGAGAGAGACAGTCTTACTGAAAGCATATAAAG 452  
Qy 181 GTATCCCAAAATTCAGATT 200  
Db 453 TTGTATCCTAGTCGAGATT 472

RESULT 11  
US-09-954-531-16  
Sequence 16, Application US/09954531  
Patent No. US20020165180A1  
GENERAL INFORMATION:  
APPLICANT: Weaver, Zoe  
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance  
FILE REFERENCE: 689290-77  
CURRENT APPLICATION NUMBER: US/09/954,531  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: US/60/233,133  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US/60/234,009  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,034  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,509  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US/60/234,567  
PRIOR FILING DATE: 2000-09-22  
NUMBER OF SEQ ID NOS: 1392  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 16  
LENGTH: 3076  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-954-531-16

Query Match 27.5%; Score 56; DB 9; Length 3076;  
Best Local Similarity 55.0%; Pred. No. 4.5e-08;  
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACACTTTTGCTAATTTTCCAACTGGTAGTCCTGTTTTCAGCATCA 60  
Db 809 GAACGTGTACCGAATGCTCTACGTATTCACACTTTTCTGCTGGGTTCCCTGCTCAGAAAGG 868  
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGGTGAAGAGATACCGTCCGGTGGCTTTAGT 120  
Db 869 AGTCTTGCTGCTGGTGTCTTATACACTGGTGTGAATGACAGGTCAAATGCTTCTGT 928  
Qy 121 TGTCTATGACGTGTAGATAGATGGAATATGGAGACTCAGCAGTGTGGAAGACACAGGAAA 180  
Db 929 TGTGCTCTGATGCTGGATACTGGAAGAGAGAGACAGTCTTACTGAAAGCATATAAAG 988  
Qy 181 GTATCCCAAAATTCAGATT 200  
Db 989 TTGTATCCTAGTCGAGATT 1008

RESULT 12

US-09-954-456-1635  
Sequence 1635, Application US/09954456  
Patent No. US20020115057A1  
GENERAL INFORMATION:  
APPLICANT: Young, Paul  
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using  
FILE REFERENCE: 689290-76  
CURRENT APPLICATION NUMBER: US/09/954,456  
CURRENT FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: US/60/233,617  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US/60/234,052  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,923  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: US/60/235,134  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: US/60/235,637  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/60/235,638  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/60/235,711  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,720  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,840  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,863  
PRIOR FILING DATE: 2000-09-27  
NUMBER OF SEQ ID NOS: 2276  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1635  
LENGTH: 3076  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-954-456-1635

Query Match 27.5%; Score 56; DB 10; Length 3076;  
Best Local Similarity 55.0%; Pred. No. 4.5e-08;  
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
Qy 1 GAGTTTAATAGATTAAACACTTTTGCTAATTTTCCAACTGGTAGTCCTGTTTTCAGCATCA 60  
Db 809 GAACGTGTACCGAATGCTCTACGTATTCACACTTTTCTGCTGGGTTCCCTGCTCAGAAAGG 868  
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGGTGAAGAGATACCGTCCGGTGGCTTTAGT 120  
Db 869 AGTCTTGCTGCTGGTGTCTTATACACTGGTGTGAATGACAGGTCAAATGCTTCTGT 928

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QY 121 TGTATGACGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 929 TGTGGCTGTAGCTGGATTAAGTGGAAAGAGAGAGACAGTCTACTGAAAGCATATAAAG 988
QY 181 GTATCCCAAAATTCAGATT 200
Db 989 TTGTATCCTAGCTGCAGATT 1008

RESULT 13
us-09-974-592-f
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
; US-09-974-592-5

Query Match 27.5%; Score 56; DB 10; Length 6669;
Best Local Similarity 55.0%; Pred. No. 6.7e-08;
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTGCTAAATTTTCCAACTGGTAGTCCCTGTTTCAGCATCA 60
Db 4305 GAACGTGTACCGAATGCTACGATATCCACTTTTCTGCTGGGTTCCCTGCTCAGAAAGG 4364
QY 61 ACACGTGGCAGCAGCAGGCTTTCTTTATCTAGTGTGAAGAGATACCGTGGGTCCTTTAGT 120
Db 4365 AGCTGTGCTGCTGCTGGTCTTATATACACTGGTGTGAATGACAAGTCAAAATGCTTCTGT 4424
QY 121 TGTATGACGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 4425 TGTGGCTGTAGCTGGATTAAGTGGAAAGAGAGAGACAGTCTACTGAAAGCATATAAAG 4484
QY 181 GTATCCCAAAATTCAGATT 200
Db 4485 TTGTATCCTAGCTGCAGATT 4504

RESULT 14
US-09-201-936-7
; Sequence 7, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
```

```
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS.
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: variation
; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
; US-09-201-936-7

Query Match 27.4%; Score 55.8; DB 9; Length 2580;
Best Local Similarity 54.7%; Pred. No. 4.8e-08;
Matches 111; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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QY 61 ACACGTGGCAGCAGCAGGCTTTCTTTATCTAGTGTGAAGAGATACCGTGGGTCCTTTAGT 120
Db 433 AGCTGTGCTGCTGCTGGTCTTATATATATATGCTGTGAATGACAAGTCAAAATGCTTCTGT 492
QY 121 TGTATGACGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 493 TGTGGCTGTAGCTGGATTAAGTGGAAAGAGAGACAGTCTACTGAAAGCATATAAAG 552
QY 181 GTATCCCAAAATTCAGATT 203
Db 553 CTATATCCTAGCTGTAGCTTTAT 575

RESULT 15
US-09-880-107-3354
; Sequence 3354, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3354
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U37547
; US-09-880-107-3354
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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8: em\_hic:\*  
9: gb\_esti:\*  
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11: gb\_hic:\*  
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14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	170.4	83.5	698	10	BB653654
5	129	63.2	822	12	BG502660
6	111.4	54.6	575	13	BM489612

7	103	50.5	676	13	BI392530
8	93.2	45.7	603	9	AL646185
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15	68.4	33.5	1130	13	BM553272
16	66.8	32.7	742	13	BI829221
17	66.8	32.7	1020	13	BM554544
18	66.4	32.5	557	13	BI475879
19	66.4	32.5	562	13	BI706974
20	66.4	32.5	565	13	BI706975
21	66.4	32.5	676	12	BF156225
22	64.8	31.8	574	13	BI706911
23	64.4	31.6	624	14	BQ552033
24	64.2	31.5	746	9	AF160669
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38	57	27.9	613	14	BQ391082
39	57	27.9	644	14	BQ389388
40	56	27.5	590	10	AW500255
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## ALIGNMENTS

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AL713196  
VERSION  
AL713196.1  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

529 bp mRNA linear EST 22-MAR-2002  
DKFZp686M1895\_r1 686 (synonym: hlccc) Homo sapiens cDNA clone  
DKFZp686M1895 5', mRNA sequence.  
GI:19696552

Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 529)  
Bloecher,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann  
/S.  
EST (Bloecher,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and  
Wiemann,S.)  
Unpublished (1999)  
Contact: Bloecker H  
MIPS  
Am Klopferstritz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ): Email s.wiemann@dkfz-heidelberg.de;  
Sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No s1 sequence available.  
This clone (DKFZp686M1895) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

Location/Qualifiers

source

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/db\_xref="taxon:9606"  
/clone="DF2686MI95"  
/clone\_lib="686 (synonym: hlcc3)"  
/tissue\_type="human skeletal muscle"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="vector: pTriplEx2; Site\_1: SfiII; Site\_2: SfiIIB;  
cdna collection"

BASE COUNT 165 a 96 c 126 g 142 t

## ORIGIN

Query Match 100.0%; Score 204; DB 9; Length 529;  
Best Local Similarity 100.0%; Pred. No. 8.1e-54; Indels 0; Gaps 0;  
Matches 204; Conservative 0; Mismatches 0;

QY 1 GAGTTTATAGATTAAACCTTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 60

Db 137 GAGTTTATAGATTAAACCTTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 196

QY 61 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 120

Db 197 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 256

QY 121 TGTATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180

Db 257 TGTATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 316

QY 181 GTATCCCCAAATTCAGATTATC 204

Db 317 GTATCCCCAAATTCAGATTATC 340

## RESULT 2

BM459898

LOCUS

DEFINITION BM459898 1041 bp mRNA linear EST 05-FEB-2002

AGENCOURT\_6422054 NIH\_MGC\_71 Homo sapiens cdna clone IMAGE:5532247

5', mRNA sequence.

ACCESSION BM459898

VERSION BM459898.1 GI:18508938

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@rs-re@mail.nih.gov

Tissue Procurement: ATCC

cdna Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12215 row: d column: 08

High quality sequence stop: 567.

Location/Qualifiers

1..1041

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5532247"

/clone\_lib="NIH\_MGC\_71"

/tissue\_type="leiomyosarcoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb.

BASE COUNT 297 a 208 c 266 g 269 t

ORIGIN

Query Match 100.0%; Score 204; DB 13; Length 1041;

Best Local Similarity 100.0%; Pred. No. 1.1e-53;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTATAGATTAAACCTTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 60

Db 142 GAGTTTATAGATTAAACCTTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 201

QY 61 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 120

Db 202 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 261

QY 121 TGTATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180

Db 262 TGTATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 321

QY 181 GTATCCCCAAATTCAGATTATC 204

Db 322 GTATCCCCAAATTCAGATTATC 345

## RESULT 3

BQ423165

LOCUS

DEFINITION BQ423165 852 bp mRNA linear EST 23-MAY-2002

AGENCOURT\_7761069 NIH\_MGC\_72 Homo sapiens cdna clone IMAGE:6062005

5', mRNA sequence.

ACCESSION BQ423165

VERSION BQ423165.1 GI:21118480

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@rs-re@mail.nih.gov

Tissue Procurement: ATCC/DCFD/PTP

cdna Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13332 row: m column: 14

High quality sequence stop: 503.

Location/Qualifiers

1..852

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:6062005"

/clone\_lib="NIH\_MGC\_72"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."

Location/Qualifiers

210 a 191 c 242 g 209 t

BASE COUNT

ORIGIN

Query Match 94.6%; Score 193; DB 14; Length 852;

Best Local Similarity 99.5%; Pred. No. 3.1e-50;

Matches 204; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GAGTTTATAGATTAAACCTTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 60



CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCMI449 row: c column: 23  
 High quality sequence stop: 670.  
 Location/Qualifiers

FEATURES  
 source  
 1. 822  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4657102"  
 /clone\_lib="NIH\_MGC\_61"  
 /tissue\_type="embryonal carcinoma"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgccctggcc); Site\_2: SfiI (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-dT(30)BN-3' (where B = A, C, G or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

BASE COUNT 236 a 161 c 201 g 222 t 2 others

Query Match 63.2%; Score 129; DB 12; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-30;  
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 GGGTTCTTTTACTGGTGAAGGAGATACCGTGGCGTCTTGTAGTGTGTCATGCACCTGTA 135  
 Db 1 GGGTTCTTTTACTGGTGAAGGAGATACCGTGGCGTCTTGTAGTGTGTCATGCACCTGTA 60

Qy 136 GATAGATGGCAATATGGAGACTACAGTTGGAGACACAGAAAGTATCCCAATATGC 195  
 Db 61 GATAGATGGCAATATGGAGACTACAGTTGGAGACACAGAAAGTATCCCAATATGC 120

Qy 196 AGATTATC 204  
 Db 121 AGATTATC 129

RESULT 6  
 BM489612 575 bp mRNA linear EST 07-FEB-2002  
 LOCUS pgm2n.pk011.h2 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk011.h2 5' similar to gb|AA47170.1|AF451854.1 (AF451854) inhibitor of apoptosis protein 3 [Gallus gallus], mRNA sequence.  
 ACCESSION BM489612  
 VERSION BM489612.1 GI:18610543  
 KEYWORDS EST.  
 SOURCE chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 575)  
 AUTHORS Cogburn, L.A. and Monsonego-Ornan, E.  
 TITLE ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Larry A. Cogburn  
 University of Delaware  
 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302-831-1335

Fax: 302-831-2822  
 Email: [cogburn@udel.edu](mailto:cogburn@udel.edu), [www.chickest.udel.edu](http://www.chickest.udel.edu).  
 Location/Qualifiers

FEATURES  
 source  
 1. 575  
 /organism="Gallus gallus"  
 /strain="Commercial broiler and Ottawa Res. Centre Strains 90 & 21"  
 /db\_xref="taxon:9031"  
 /clone="pgm2n.pk011.h2"  
 /clone\_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"  
 /sex="Male and Female"  
 /tissue\_type="Breast muscle, leg muscle and epiphyseal growth plate"  
 /dev\_stage="Breast, leg; Embryo(d19); post-hatch(1d,1.3,5,7,9,11 weeks); growth plate(1d,7d,14d post-hatch)"  
 /lab\_host="E. coli EMDH10B"  
 /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

BASE COUNT 144 a 131 c 152 g 145 t 3 others

Query Match 54.6%; Score 111.4; DB 13; Length 575;  
 Best Local Similarity 73.6%; Pred. No. 1.9e-24;  
 Matches 142; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 11 GATTAAAACTTTTGTCTTAATTTTCAAGGTAGTCTCTTTCAGCATCAACACTGGCAC 70  
 Db 138 GACTAGGAACCTTTGTGGAGTTTCCCATGATGTCAGCTTCAGCATGCGTAGCTC 197

Qy 71 GAGCAGGGTTCTTTTACTACTGTTGAAGGAGATACCGTGGCGTCTTACTGTCTATGCAG 130  
 Db 198 GAGCTGGCTTTGTTTATCTACTGGAGAAGGTGATAAGTCAAGTGCCTTCAGTGCATGTAA 257

Qy 131 CTGTAGATAGATGGCAATATGGAGACTACAGTCTGGAGACACAGAAAGTATCCCA 190  
 Db 258 CTGTTGAAGGATGGAGCTTGGGATTCGCAATTGACAGACACAAAACCTTTCCCC 317

Qy 191 ATTGCAGATTAT 203  
 Db 318 ATTGCAGATTAT 330

RESULT 7  
 BI392530 676 bp mRNA linear EST 06-AUG-2001  
 LOCUS pgpin.pk008.d6 Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus gallus cDNA clone pgpin.pk008.d6 5' similar to gb|AA22969.1|AF183429.1 (AF183429) inhibitor of apoptosis protein 3 [Rattus norvegicus], mRNA sequence.  
 ACCESSION BI392530  
 VERSION BI392530.1 GI:15085812  
 KEYWORDS EST.  
 SOURCE chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 676)  
 AUTHORS Porter, T.E. and Cogburn, L.A.  
 TITLE ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA library USDA/IFAFS Animal Genome Project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Larry A. Cogburn  
 University of Delaware  
 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302-831-1335  
 Fax: 302-831-2822  
 Email: [cogburn@udel.edu](mailto:cogburn@udel.edu), [www.chickest.udel.edu](http://www.chickest.udel.edu).  
 Location/Qualifiers

FEATURES



BASE COUNT	165 a	131 c	150 g	156 t	1 others	
ORIGIN						
Query Match			45.7%	Score 93.2;	DB 9;	Length 503;
Best Local Similarity			67.5%;	Pred. No. 1.2e-18;		
Matches 131;			Conservative	0;	Mismatches 63;	Indels 0; Gaps 0;
QY	10	AGATTAAAACTTTTGCTAAATTTTCCAAAGTGCTAGTCTCTGTTCCAGCATCAACACTGGCA	69			
DB	163	AGACTGGCGTCTTTGGTAACTTCCCAAGTAGGTACCGGGTCTCTGCTCCAGCACTAGCG	222			
QY	70	CGACGAGGGTTCCTTTATCTACTGGTGAAGGAGATACCGGTGCGGTGCTTTAGTTGTCATGCA	129			
DB	223	CGGCGCGCTCTATTACACTGGAGATGGAGATCGAGTCAAGTGTTTTAGCTGCTGGCT	282			
QY	130	GCTGTAGATAGATCGAATATGGAGACTACACAGTCTGGAGACACAGAGAAAGTATPCCCA	189			
DB	283	ATGCTTGAAGCTGGCAGCATGGAGACACGCAATTTGGCAAGCAGCGGAAAAATATCCCA	342			
QY	190	AATTGCAGATTAT	203			
DB	343	AACTGTAATTAT	356			
RESULT 9						
LOCUS	BJ096099		593 bp	mRNA	linear	EST 12-DEC-2001
DEFINITION	BJ096099	NIBB Mochii normalized xenopus early gastrula library				
ACCESSION	BJ096099	Xenopus laevis cDNA clone XL152k19 5', mRNA sequence.				
VERSION	BJ096099.1	GI:175956868				
KEYWORDS	EST.					
SOURCE	African clawed frog.					
ORGANISM	Xenopus laevis					
	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;					
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;					
	Xenopodinae; Xenopus.					
REFERENCE	1. (bases 1 to 593)					
AUTHORS	Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.					
TITLE	Expressed genes in X. laevis embryo					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Tadasu Shin-i					
	Center For Genetic Resource Information					
	National Institute of Genetics					
	1111 Yata, Mishima, Shizuoka 411-8540, Japan					
	Tel: 81-559-81-6856					
	Fax: 81-559-81-6855					
	Email: tshini@genes.nig.ac.jp.					
FEATURES	Location/Qualifiers					
source	1..593					
	/organism="Xenopus laevis"					
	/db_xref="taxon:8355"					
	/clone="XL152k19"					
	/clone_lib="NIBB Mochii normalized xenopus early gastrula library"					
	/dev_stage="stage 10.5"					
	/note="vector: pBSRN3; Site.1: NotI; Site.2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."					
BASE COUNT	175 a	129 c	137 g	152 t		
ORIGIN						
Query Match			44.9%	Score 91.6;	DB 13;	Length 593;
Best Local Similarity			67.0%;	Pred. No. 3.7e-18;		





LOCUS BG773530 756 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602720264F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4837478 5',  
 mRNA sequence.  
 ACCESSION BG773530  
 VERSION BG773530.1 GI:14084183  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 756)  
 TITLE NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-r@mail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10769 row: o column: 15  
 High quality sequence stop: 740.  
 FEATURES  
 source  
 1..756  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4837478"  
 /clone\_lib="NIH\_MGC\_97"  
 /lab\_host="DH10B"  
 /note="Organ: testis; Vector: pBluescriptR (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
 size-selected for average insert size 2.2 kb and  
 normalized to ROT 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constituted by M. Brownstein (NIH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."  
 BASE COUNT 166 a 181 c 245 g 163 t 1 others  
 ORIGIN  
 Query Match 33.8%; Score 69; DB 12; Length 756;  
 Best Local Similarity 64.7%; Pred. No. 6e-11;  
 Matches 132; Conservative 0; Mismatches 46; Indels 26; Gaps 1;  
 QY 1 GAGTTTAAATAGATTAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCTGTTTCAGCATCA 60  
 DB 384 GAGATTATAGATCAAAACAGTTTCTGCTGCTTTCAGTGTGGCCCTCGGCGCATCG 443  
 QY 61 ACACCTGGCAGCAGGAGGTTTCTTTATACGTGTGAAGAGATACCGTGGGTCCTTTAGT 120  
 DB 444 GCGC-----GNTGAGGAGAGCGCCCTGGGGGCGCTTAGC 477  
 QY 121 TGTCTAGCAGCTGTAGATAGATGGCAATATGGAGACTCAGAGTGGAGACACAGGAAA 180  
 DB 478 TGCCCTGAAGCGGTAGACAGGTGGCAACGTGGGGCTCAGGAGTTGACAAACACAGAAA 537  
 QY 181 GTATCCCAAAATTCGAGATTATC 204  
 DB 538 GCAGCGCCGAATTCGAGGTTTATC 561  
 RESULT 15  
 BM553272  
 LOCUS BM553272 1130 bp mRNA linear EST 20-FEB-2002  
 DEFINITION AGENCOURT\_6542515 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5742924  
 5', mRNA sequence.  
 ACCESSION BM553272  
 VERSION BM553272.1 GI:18791860

KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1130)  
 TITLE NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12761 row: n column: 13  
 High quality sequence stop: 691.  
 FEATURES  
 source  
 1..1130  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5742924"  
 /clone\_lib="NIH\_MGC\_119"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC Library."  
 BASE COUNT 257 a 267 c 343 g 261 t 2 others  
 ORIGIN  
 Query Match 33.5%; Score 68.4; DB 13; Length 1130;  
 Best Local Similarity 64.7%; Pred. No. 1.1e-10;  
 Matches 132; Conservative 0; Mismatches 46; Indels 26; Gaps 1;  
 QY 1 GAGTTTAAATAGATTAAACCTTTTCTTAATTTTCCAAAGTGTAGTCCTGTTTCAGCATCA 60  
 DB 391 GAGATTATAGATCAAAACAGTTTCTGCTTTCAGGTTGGGCTCCCTCGGCGCATCG 450  
 QY 61 ACACCTGGCAGCAGGAGGTTTCTTTATACGTGTGAAGAGATACCGTGGGTCCTTTAGT 120  
 DB 451 GCGC-----GTTGAGGAGAGCGCCCTGGGGGCGCTTAGC 484  
 QY 121 TGTCTAGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180  
 DB 485 TGCCCTGAAGCGGTAGACAGGTGGCAACGTGGGGCTCAGGAGTTGACAAACACAGAAA 544  
 QY 181 GTATCCCAAAATTCGAGATTATC 204  
 DB 545 GCAGCGCCGAATTCGAGGTTTATC 568  
 Search completed: April 16, 2003, 00:54:50  
 Job time : 983.083 Secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 seconds  
(without alignments)  
5753.635 Million cell updates/sec

Title: US-09-654-743-46  
Perfect score: 204  
Sequence: 1 gaagaagctagattaaagtc.....ttcctaattgctctttgtt 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_cm.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgt\_mus.\*
- 34: em\_hgt\_pln.\*
- 35: em\_hgt\_rod.\*
- 36: em\_hgt\_mam.\*
- 37: em\_hgt\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hgtgo\_hum.\*
- 40: em\_hgtgo\_mus.\*
- 41: em\_hgtgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	204	100.0	1659	6	E31042
2	204	100.0	1659	9	HSU32974
3	204	100.0	2086	9	BC032729
4	204	100.0	2540	6	ARI03281
5	204	100.0	2540	6	AX412118
6	204	100.0	2540	9	HSU45880
7	204	100.0	3000	6	AX412131
8	204	100.0	5232	6	ARI06397
9	204	100.0	5232	6	ARI16699
10	204	100.0	133391	9	HSU315G1
11	204	100.0	201197	2	HS424J12
12	193	94.6	2404	6	AX429575
13	172	84.3	2100	6	AX412124
14	172	84.3	2691	6	ARI06400
15	172	84.3	2691	6	ARI16702
16	172	84.3	2691	10	MMU88990
17	170.4	83.5	1988	10	MMU36842
18	167.2	82.0	2032	10	AF304333
19	167.2	82.0	2468	10	AB033366
20	167.2	82.0	3032	10	AF304334
21	165.6	81.2	1491	10	AF183429
22	165.6	81.2	1758	6	AX370787
23	164	80.4	1758	6	AX370789
24	164	80.4	2032	9	AF420440
25	164	80.4	4993	6	AX104968
26	164	80.4	4993	9	AF164682
27	164	80.4	144301	9	AC010467
28	164	80.4	165662	9	AC092070
29	141	69.1	184439	2	AP003085
30	141	69.1	187568	9	AP002967
31	138.4	67.8	7990	6	AX281265
32	138.4	67.8	7990	6	AX345060
33	132.6	65.0	1740	5	AF451854
34	129.4	63.4	7990	6	AX281266
35	129.4	63.4	7990	6	AX345061
36	84.6	41.5	2563	9	HUMSCP8
37	84.6	41.5	2601	6	ARI29833
38	84.6	41.5	2676	6	AX412120
39	84.6	41.5	2916	9	HSU45878
40	84.6	41.5	3076	6	AR076287
41	84.6	41.5	3076	6	AX330574
42	84.6	41.5	3076	6	AX334153
43	84.6	41.5	3076	9	HSU37546
44	84.6	41.5	3734	6	AX055871
45	84.6	41.5	3734	6	AX472621

ALIGNMENTS

RESULT 1

E31042	E31042	Method for screening substance inhibiting binding to XIAP.	Linear	PAT 18-JUN-2001
LOCUS	E31042	Method for screening substance inhibiting binding to XIAP.	DNA	
DEFINITION	E31042	Method for screening substance inhibiting binding to XIAP.		
ACCESSION	E31042	Method for screening substance inhibiting binding to XIAP.		
VERSION	E31042.1	GI:13017307		
KEYWORDS	JP 1999326328-A/2.			
SOURCE	unidentified.			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 1659)			
AUTHORS	Kunihiro,M.			
TITLE	Method for screening substance inhibiting binding to XIAP			
JOURNAL	Patent: JP 1999326328-A 2 26-NOV-1999;			
	KUNIHIRO MATSUMOTO			

```

COMMENT OS Unidentified
PN JP 199328328-A/2
PD 26-NOV-1999
PF 13-MAY-1998 JP 1998130378
PR KUNIHIO MATSUMOTO
PC G01N33/536, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/22,
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A61K37/02, PC A61K37/02,
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CC Key Location/Qualifiers
FT CDS 82..1572.
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.4e-56;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 628 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTTGGTACCAGTGCAGTGTCTTGT 687
QY 121 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGTCAGACACAGGCGA 180
DB 588 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGTCAGACACAGGCGA 747
QY 181 CACTTTCCTAATGCTCTCTTTGTT 204
DB 748 CACTTTCCTAATGCTCTCTTTGTT 771
RESULT 2
HSU32974 1659 bp mRNA linear PRI 12-JUN-1996
LOCUS Human IAP-like protein ILP mRNA, complete cds.
DEFINITION
ACCESSION U32974
VERSION U32974.1 GI:1016687
KEYWORDS apoptosis; ring finger; zinc finger.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
Gilfillan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
TITLE A conserved family of cellular genes related to the baculovirus iap
gene and encoding apoptosis inhibitors
JOURNAL EMBO J. 15 (11), 2685-2694 (1996)
MEDLINE 96256286
PUBMED 8654366
REFERENCE
AUTHORS Duckett,C.S. and Thompson,C.B.
TITLE Direct Submission
JOURNAL Submitted (01-AGU-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
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source Location/Qualifiers
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DB 568 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 627
QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTTGGTACCAGTGCAGTGTCTTGT 120
DB 628 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTTGGTACCAGTGCAGTGTCTTGT 687
QY 121 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGTCAGACACAGGCGA 180
DB 588 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGTCAGACACAGGCGA 747
QY 181 CACTTTCCTAATGCTCTCTTTGTT 204
DB 748 CACTTTCCTAATGCTCTCTTTGTT 771
RESULT 3
BC032729 2086 bp mRNA linear PRI 27-JUN-2002
LOCUS Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369
DEFINITION
IMAGE:5532247, mRNA, complete cds.
ACCESSION BC032729
VERSION BC032729.1 GI:21619763
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC); Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov

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Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_msc@hgrl.nih.gov/  
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAP Plate: 69 Row: j Column: 18  
 This clone was selected for full length sequencing because it  
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# FEATURES

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RESULT 4  
 AR103281  
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DEFINITION Sequence 1 from patent US 6087173.  
 ACCESSION AR103281  
 VERSION AR103281.1 GI:12814869  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 2540)  
 AUTHORS Bennett, C. Frank., Ackermann, E.J. and Cowser, L.M.  
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression  
 JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
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 DB 700 CACTTTCCTAATGCTCTCTTTGTT 723  
 RESULT 5  
 AX412118 2540 bp DNA linear PAT 14-JUN-2002  
 LOCUS  
 Sequence 218 from Patent WO0226968.  
 DEFINITION  
 AX412118  
 ACCESSION  
 AX412118.1 GI:21444581  
 VERSION  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1  
 AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
 TITLE Antisense iap nucleic acids and uses thereof  
 JOURNAL Patent: WO 0226968-A 218 04-APR-2002;  
 University of Ottawa (CA); Asgerta Therapeutics Inc. (CA)  
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RESULT 6  
 HSU45880 2540 bp mRNA linear PRI 16-FEB-1996  
 LOCUS Human x-linked inhibitor of apoptosis protein XIAP mRNA, complete  
 DEFINITION cds.  
 ACCESSION U45880  
 VERSION U45880.1 GI:1184319  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2540)  
 Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,  
 Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., MacKenzie, A.  
 and Korneluk, R. G.  
 TITLE Suppression of apoptosis in mammalian cells by NAIP and a related  
 family of IAP genes  
 JOURNAL Nature 379 (6563), 349-353 (1996)  
 MEDLINE 96149249  
 PUBMED 8552191  
 REFERENCE 2 (bases 1 to 2540)  
 Baird, S.D.  
 AUTHORS Direct Submission  
 TITLE Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of  
 Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1,  
 Canada  
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 ACCESSION AX412131  
 VERSION AX412131.1 GI:21444588  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1  
 Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
 Antisense IAP nucleic acids and uses thereof  
 TITLE Patent: WO 0226968-A 231 04-APR-2002;  
 JOURNAL University of Ottawa (CA); Aegera Therapeutics Inc. (CA)  
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 /db\_xref="taxon:9606"  
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QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120  
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RESULT 8  
 ARI06397 5232 bp DNA linear PAT 14-FEB-2001  
 LOCUS ARI06397  
 DEFINITION Sequence 3 from patent US 6107041.  
 ACCESSION ARI06397  
 VERSION ARI06397.1 GI:12820927  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.



```

REFERENCE 1 (bases 1 to 5232)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 3 22-AUG-2000;
FEATURES
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BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
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Db 520 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTTGT 120
Db 580 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTTGT 639
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGCCTGGTCAGAACACAGCGCA 180
Db 640 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGCCTGGTCAGAACACAGCGCA 699
QY 181 CACTTTCCTTAATTCCTTTCTTTTGT 204
Db 700 CACTTTCCTTAATTCCTTTCTTTTGT 723

RESULT 9
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LOCUS ARL16699 5232 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6133437.
ACCESSION ARL16699
VERSION ARL16699.1 GI:14097021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5232)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;
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Db 520 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTTGT 120
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QY 181 CACTTTCCTTAATTCCTTTCTTTTGT 204
Db 700 CACTTTCCTTAATTCCTTTCTTTTGT 723

Db 700 CACTTTCCTTAATTCCTTTCTTTTGT 723

RESULT 10
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LOCUS HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000
DEFINITION Human DNA sequence from clone RPl-315G1 on chromosome Xq24-25. Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene, ESTs, STSSs, GSSs and a putative cpg island, complete sequence.
ACCESSION AL121601
VERSION AL121601.13 GI:7159760
KEYWORDS HUG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 133391)
AUTHORS Grafham,D.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Mar 6, 2000 this sequence version replaced gi:6983378. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C.elegans/Wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RPl-315G1 is from the library RPl-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2 This sequence is the entire insert of clone RPl-315G1 The true right end of clone RP6-30A23 is at 100 in this sequence.
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DEFINITION PROGRESS ***, 15 unordered pieces.
ACCESSION Z82207
VERSION Z82207.3 GI:12331276
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 201197)
AUTHORS Grafham, D.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Jan 22, 2001 this sequence version replaced gi:100451116.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: G0424J12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 74% of reads
Sequencing method: Plasmid; 108752; 25% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator ABI; 96% of reads
Chemistry: Dye-primer-amerham; 2% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 194333 bases at least Q40
Consensus quality: 196512 bases at least Q30
Consensus quality: 198047 bases at least Q20
Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 4155 4254: gap of 100 bp
* 4255 18703: contig of 14449 bp in length
* 18704 18803: gap of 100 bp
* 18804 20941: contig of 2138 bp in length
* 20942 21041: gap of 100 bp
* 21042 34907: contig of 13866 bp in length
* 34908 35012: gap of 105 bp
* 35013 37508: contig of 2496 bp in length
* 37509 37608: gap of 100 bp
* 37609 52739: contig of 15131 bp in length
* 52740 52839: gap of 100 bp
* 52840 56933: contig of 4094 bp in length
* 56934 57033: gap of 100 bp
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* 88246 88346: gap of 101 bp
* 88347 93386: contig of 5040 bp in length

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* 147918 148017: gap of 100 bp
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* 190825 190958: gap of 135 bp
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SOURCE Unknown.

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ORGANISM      Unknown.
Unclassified.
REFERENCE     1. (bases 1 to 2691)
AUTHORS      Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and
              Pratt,C.
TITLE        Modulation of IAPs for the treatment of proliferative diseases
JOURNAL      Patent: US 6133437-A 9 17-OCT-2000;
FEATURES     Location/Qualifiers
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                                Location=unknown
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Search completed: April 15, 2003, 23:23:52  
Job time : 1068.86 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 136.354 Seconds

(without alignments)

3369.223 Million cell updates/sec

Title: US-09-654-743-46

Perfect score: 204

Sequence: 1 gaagaactagattaaagtc.....ttcctaattgtttttgtt 204

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	204	100.0	2540	18	AAZ70836 Human apoptosis in
3	204	100.0	2540	21	AAA64901 Human X-linked inh
4	204	100.0	2540	24	ABK93869 Human CDNA encodin
5	204	100.0	3000	24	ABK93875 Human CDNA encodin
6	204	100.0	5232	19	AAV55038 Human XIAP coding
7	193	94.6	2404	24	AAK99405 DNA of APP related
8	172	84.3	2100	18	AAZ70839 Mouse apoptosis in
9	172	84.3	2100	24	ABK93872 Mouse CDNA encodin

10	172	84.3	2691	19	AAV55041
11	170.4	83.5	1988	18	AAZ72710
12	165.6	81.2	1758	24	ABK14677
13	164	80.4	1559	24	ABK13197
14	164	80.4	1758	24	ABK14678
15	164	80.4	4993	22	AAZ03581
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18	129.4	63.4	7990	24	ABL54308
19	129.4	63.4	7990	24	ABL33159
20	84.6	41.5	2601	18	AAZ61591
21	84.6	41.5	2666	18	AAZ70837
22	84.6	41.5	2676	24	ABK93870
23	84.6	41.5	3076	18	AAZ72712
24	84.6	41.5	3076	20	AAZ41005
25	84.6	41.5	3076	20	AAZ22096
26	84.6	41.5	3076	24	ABL62746
27	84.6	41.5	3076	24	ABL66325
28	84.6	41.5	3734	22	AAZ09972
29	84.6	41.5	3734	24	ABK53387
30	84.6	41.5	6669	19	AAV55039
31	84.6	41.5	6669	24	ABK93876
32	74.4	36.5	2862	18	AAZ61592
33	74.4	36.5	3151	19	AAV55043
34	72.8	35.7	2416	18	AAZ70841
35	72.8	35.7	2416	24	ABK93874
36	70.2	34.4	2291	22	AAZ08025
37	70.2	34.4	2580	18	AAZ70838
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40	70.2	34.4	3532	18	AAZ72711
41	70.2	34.4	3532	20	AAZ22143
42	70.2	34.4	3532	24	ABK96857
43	70.2	34.4	3732	19	AAV55040
44	68.6	33.6	1435	17	AAZ43709
45	62.8	30.8	2474	18	AAZ70840

#### ALIGNMENTS

RESULT 1

AAZ48862

ID AAZ48862 standard; cDNA; 1659 BP.

AC AAZ48862;

XX 24-MAR-2000 (first entry)

XX Human XIAP coding sequence.

DE Human XIAP coding sequence.

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;

KW transforming growth factor-beta activated kinase 1; monocyte migration;

KW TAK1 binding protein 1; extracellular matrix protein production;

KW cell growth inhibitor; beta-amyloid protein deposition;

KW immunosuppression; Transforming growth factor-beta; ds.

XX Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-0130378.

XX 13-MAY-1998; 98JP-0130378.

XX (MATS/) MATSUMOTO K.

XX WPI; 2000-078337/07.

XX P-PSDB; AAY59451.

XX Screening a substance which inhibits combination of the X-linked

PT

Murine XIAP coding  
Mouse inhibitor of  
Human inhibitor of  
Human testes speci  
Human inhibitor of  
Human IAP-like pro  
Chemically treated  
Human immune syste  
Chemically treated  
Human immune syste  
Human c-IAP2. Hom  
Human apoptosis in  
Human cDNA encodin  
Human inhibitor of  
Human cellular inh  
Breast cancer rela  
Lung cancer relate  
Human APl2-MT chl  
DNA encoding cysti  
Human HIAP-1 codin  
Human cDNA encodin  
Murine c-IAP. Mus  
Murine HIAP-2 codi  
Mouse apoptosis in  
Mouse cDNA encodin  
Angiotensin conver  
Human apoptosis in  
Human cDNA encodin  
Human c-IAP1. Hom  
Human inhibitor of  
Human cellular inh  
Gene #3355 used to  
Human HIAP-2 codin  
Human inhibitor of  
Mouse apoptosis in

inhibitor of apoptosis protein -

PT inhibitor of apoptosis protein -  
 XX Disclosure; Page 28-30; 43pp; Japanese.  
 XX This sequence encodes the human XIAP protein.  
 CC The invention relates to a method for screening a substance inhibiting  
 CC the formation of a complex between XIAP and TAB1, in which X-linked  
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
 CC activated kinase 1 (TAK1) binding protein (TAB1) and a substance to be  
 CC tested are contacted with each other and then the presence or formation  
 CC of a complex between XIAP and TAB1 is detected. The substance can be used  
 CC as a drug for extracellular matrix protein production enhancement, cell  
 CC growth inhibition, monocyte migration, physiologically active substance  
 CC induction, immunosuppression, and beta-amyloid protein deposition. A  
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as  
 CC well as between XIAP and TGF-beta (transforming growth factor-beta) type  
 CC I and/or type II receptor is useful as a drug.  
 XX  
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;

Query Match 100.0%; Score 204; DB 21; Length 1659;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-59;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGAAGCTAGATTAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60  
 DB 568 GAAGAAGCTAGATTAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 627  
 QY 61 GAGTTAGCAAGTGGTGGTCTTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120  
 DB 628 GAGTTAGCAAGTGGTGGTCTTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 687  
 QY 121 TGTGGTGGAAACTGAAAATTTGGAACTTGTGATCGCTGCTGCTGACACACAGGCGA 180  
 DB 688 TGTGGTGGAAACTGAAAATTTGGAACTTGTGATCGCTGCTGCTGACACACAGGCGA 747  
 QY 181 CACTTTCCTAATGCTCTTTGTT 204  
 DB 748 CACTTTCCTAATGCTCTTTGTT 771

RESULT 2  
 AA770836  
 ID AA770836 standard; cDNA; 2540 BP.  
 XX  
 AC AA770836;  
 XX

DT 02-SEP-1997 (first entry)  
 XX Human apoptosis inhibitor xiap cDNA.

DE Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
 KW ischaemia; myocardial infarction; stroke;  
 KW reperfusion injury; toxin-induced liver disease; gene therapy;  
 KW diagnosis; ds.

XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 34..1527  
 FT /\*tag= a  
 FT

PN W09706255-A2.  
 XX 20-FEB-1997.  
 XX 05-AUG-1996; 96WO-IB01022.  
 XX 22-DEC-1995; 95US-0576956.  
 PR 04-AUG-1995; 95US-0511485.  
 XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;  
 XX WPI; 1997-154262/14.  
 DR P-PSDB; AAW19581.  
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease  
 XX  
 PS Claim 12: Page 67-68; 21pp; English.  
 XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and  
 CC hiap-2 genes (AA770836-41) respectively code for a new class of  
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis  
 CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a  
 CC human foetal brain ZapII cDNA library using an X-linked sequence  
 CC tag site that shows strong homology with the conserved ring zinc  
 CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was  
 CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used  
 CC to express IAP polypeptides in cells and animals to inhibit  
 CC apoptosis, and as primers and probes to identify and isolate  
 CC additional IAP genes, as well as in methods for treating diseases  
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).  
 XX  
 SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;

Query Match 100.0%; Score 204; DB 18; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-59;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGAAGCTAGATTAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60  
 DB 520 GAAGAAGCTAGATTAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579  
 QY 61 GAGTTAGCAAGTGGTGGTCTTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120  
 DB 580 GAGTTAGCAAGTGGTGGTCTTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 639  
 QY 121 TGTGGTGGAAACTGAAAATTTGGAACTTGTGATCGCTGCTGCTGACACACAGGCGA 180  
 DB 640 TGTGGTGGAAACTGAAAATTTGGAACTTGTGATCGCTGCTGCTGACACACAGGCGA 699  
 QY 181 CACTTTCCTAATGCTCTTTGTT 204  
 DB 700 CACTTTCCTAATGCTCTTTGTT 723

RESULT 3  
 AAA64901  
 ID AAA64901 standard; DNA; 2540 BP.  
 XX  
 AC AAA64901;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX Human X-linked inhibitor of apoptosis DNA.  
 DE  
 XX X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880;  
 KW antisense; antiinflammatory; cytostatic; tumour; ds.  
 KW Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 34..1527  
 FT /\*tag= a  
 FT /product= "X-linked inhibitor of apoptosis"  
 FT  
 XX US6087173-A.  
 XX 11-JUL-2000.  
 PD  
 XX 09-SEP-1999; 99US-0392580.  
 PF

XX 09-SEP-1999; 99US-0392580.  
XX (ISIS-) ISIS PHARM INC.  
XX Bennett CF, Cowsett LM, Ackermann EJ;  
XX MPI; 2000-498201/44.  
XX P-PSDB; AAY99985.  
XX Antisense compound useful for research reagents, diagnostics,  
XX prophylaxis and for treating disorders associated with x-linked  
XX inhibitor of apoptosis, modulates expression of x-linked inhibitor of  
XX apoptosis  
XX Example 13; Column 43-48; 33pp; English.  
XX The present invention relates to antisense oligonucleotides designed to  
XX inhibit expression of the human x-linked inhibitor of apoptosis. The  
XX present sequence is the x-linked inhibitor of apoptosis DNA.  
XX Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are  
XX more effective inhibitors than unmodified oligonucleotides. The  
XX oligonucleotides may be used to inhibit x-linked inhibitor of apoptosis  
XX expression in cells and tissues in vitro. The oligonucleotides are also  
XX useful for treating animals or humans, prone to a disease associated  
XX with x-linked inhibitor of apoptosis. The oligonucleotides may also be  
XX used prophylactically to prevent infection, inflammation or tumour  
XX formation.  
XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;  
Query Match 100.0%; Score 204; DB 21; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 7.7e-59;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCTTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 60  
DB 570 GAAGAAGCTAGATTAAAGTCTTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 579  
QY 61 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTGACCAAGTCAGTCTTTTGT 120  
DB 580 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTGACCAAGTCAGTCTTTTGT 639  
QY 121 TGTGTGGAAGAACTGAAAATTTGGAACTTTGTGATCGTGTGCTGACAAACACAGCGGA 180  
DB 640 TGTGTGGAAGAACTGAAAATTTGGAACTTTGTGATCGTGTGCTGACAAACACAGCGGA 699  
QY 181 CACTTTCCTAATTGCTTCTTTGT 204  
DB 700 CACTTTCCTAATTGCTTCTTTGT 723  
RESULT 4  
ABK93869  
ID ABK93869 standard; cDNA; 2540 BP.  
XX AC ABK93869;  
XX 26-AUG-2002 (first entry)  
XX Human cDNA encoding inhibitor of apoptosis, XIAP #1.  
XX Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
XX cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
XX pancreatic cancer; embryonic development; viral pathogenesis;  
XX autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
XX lupus erythematosus; herpes virus infection; pox virus infection;  
XX adenovirus infection; proliferative disease.  
XX OS Homo sapiens.  
XX PN WO200226968-A2.  
XX

PD 04-APR-2002.  
XX 27-SEP-2001; 2001WO-CA01379.  
XX 28-SEP-2000; 2000US-0672717.  
XX (UYOT-) UNIV OTTAWA.  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX MPI; 2002-479562/51.  
XX P-PSDB; ABG65663.  
XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
XX enhancing apoptosis in a cell, for treating cancer and other  
XX proliferative diseases  
XX Disclosure; Fig 1; 135pp; English.  
XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
XX nucleic acid (I) that inhibits IAP biological activity, regardless of  
XX length of the antisense nucleic acid, the IAP proteins may be mouse  
XX or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
XX composition comprising a mammalian IAP antisense molecule and a method of  
XX enhancing apoptosis in a cell, comprising administering a negative  
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a  
XX mammal diagnosed with a proliferative disease. The method is useful for  
XX treating a patient diagnosed with a proliferative disease like cancer.  
XX The IAP antisense molecule is useful to treat, ameliorate, improve,  
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,  
XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
XX conditions where apoptosis is involved or implicated (e.g. embryonic  
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative  
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
XX virus, pox virus and adenovirus). The present sequence is a human IAP  
XX cDNA sequence.  
XX SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
Query Match 100.0%; Score 204; DB 24; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 7.7e-59;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCTTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 60  
DB 570 GAAGAAGCTAGATTAAAGTCTTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 579  
QY 61 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTGACCAAGTCAGTCTTTTGT 120  
DB 580 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTGACCAAGTCAGTCTTTTGT 639  
QY 121 TGTGTGGAAGAACTGAAAATTTGGAACTTTGTGATCGTGTGCTGACAAACACAGCGGA 180  
DB 640 TGTGTGGAAGAACTGAAAATTTGGAACTTTGTGATCGTGTGCTGACAAACACAGCGGA 699  
QY 181 CACTTTCCTAATTGCTTCTTTGT 204  
DB 700 CACTTTCCTAATTGCTTCTTTGT 723  
RESULT 5  
ABK93875  
ID ABK93875 standard; cDNA; 3000 BP.  
XX AC ABK93875;  
XX 26-AUG-2002 (first entry)  
XX Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
XX Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
XX



KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200226968-A2.  
 XX  
 XX 04-APR-2002.  
 XX  
 XX 27-SEP-2001; 2001WO-CA01379.  
 XX  
 XX 28-SEP-2000; 2000US-0672717.  
 XX  
 XX (UYOT-) UNIV OTTAWA.  
 XX (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX  
 XX WPI; 2002-479562/51.  
 XX  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 XX enhancing apoptosis in a cell, for treating cancer and other  
 XX proliferative diseases  
 XX  
 XX Example 2; Fig 15; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (i) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 3000 BP; 974 A; 452 C; 501 G; 973 T; 0 other;  
 Query Match 100.0%; Score 204; DB 24; Length 3000;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-59;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTACCCCAAGA 60  
 DB 1176 GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTACCCCAAGA 1235  
 QY 61 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACAAAGTCAGTCTTTTGT 120  
 DB 1236 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACAAAGTCAGTCTTTTGT 1295  
 QY 121 TGTGTGGAAACTGAAATAATTGGAACTTGTGATCGTGGCTGTCAGAACACAGGCGA 180  
 DB 1296 TGTGTGGAAACTGAAATAATTGGAACTTGTGATCGTGGCTGTCAGAACACAGGCGA 1355  
 QY 181 CACTTTCCTAATGCTTCTTTTGT 204  
 DB 1356 CACTTTCCTAATGCTTCTTTTGT 1379  
 RESULT 6  
 AAV55038

ID AAV55038 standard; cDNA; 5232 BP.  
 XX  
 XX AAV55038;  
 XX  
 XX 13-NOV-1998 (first entry)  
 XX  
 XX Human XIAP coding sequence.  
 XX  
 XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 34..1527  
 XX /\*tag= a  
 XX /product= XIAP  
 XX  
 XX WO9835693-A2.  
 XX  
 XX 20-AUG-1998.  
 XX  
 XX 13-FEB-1998; 98WO-IB00781.  
 XX  
 XX 13-FEB-1997; 97US-0800929.  
 XX  
 XX (UYOT-) UNIV OTTAWA.  
 XX  
 XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 XX Tsang B;  
 XX  
 XX WPI; 1998-467164/40.  
 XX P-PSDB; AAW69294.  
 XX  
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor  
 XX of IAP or NAIP polypeptide - also methods for prognosis based on  
 XX presence of IAP and NAIP, specifically applied to cancers involving  
 XX p53 mutations  
 XX  
 XX Claim 13; Fig 1; 147pp; English.  
 XX  
 CC This sequence encodes the human XIAP protein, which is an inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis;  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 XX  
 SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;  
 Query Match 100.0%; Score 204; DB 19; Length 5232;  
 Best Local Similarity 100.0%; Pred. No. 1e-58;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTACCCCAAGA 60  
 DB 520 GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTACCCCAAGA 579  
 QY 61 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACAAAGTCAGTCTTTTGT 120  
 DB 580 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACAAAGTCAGTCTTTTGT 639  
 QY 121 TGTGTGGAAACTGAAATAATTGGAACTTGTGATCGTGGCTGTCAGAACACAGGCGA 180

Db: 640 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGCTGATCAGAACACAGCGGA 699

QY 181 CACTTTCCTAAATGCTCTTTGTT 204  
 Db 700 CACTTTCCTAAATGCTCTTTGTT 723

## RESULT 7

AAK99405  
 ID AAK99405 standard; DNA; 2404 BP.

XX AAK99405;  
 XX 27-JUN-2002 (first entry)

XX DNA of APP related human homologue hCP35211.

DE Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;  
 KW amyloid precursor protein; tissue-specific expression control; human APP;  
 KW APP pathway modulator; gene therapy; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 692..1528  
 CDS /\*tag= a

FT /product= "Protein of human homologue hCP35211"  
 FT /note= "No start codon"

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-BF11345.

XX 29-SEP-2000; 2000US-236893P.

XX 14-JUN-2001; 2001US-298309P.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-BEFLINDUNGEN VERW GES MBH.

XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;  
 PI Reinhardt MWM, Zusman S;

XX WPI; 2002-315796/35.

XX P-PSDB; AAO20511.

XX New transgenic fly, containing DNA encoding an Abeta portion of human  
 PT APP, useful for identifying agents which modulate the APP pathway and  
 PT which can be used to treat Alzheimer's disease -

XX Example 4; Page 111; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA  
 CC encoding a polypeptide having the Abeta portion of human amyloid  
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence  
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in  
 CC the specification. The DNA sequence is operably linked to a tissue-  
 CC specific expression control sequence. Expression of the sequence gives  
 CC the fly an altered phenotype. The purpose of the invention is for  
 CC identifying agents that inhibit or promote the expression and/or function  
 CC of genes or encoded polypeptides which modify the APP pathway. The agent  
 CC is a compound, triple helix DNA, antisense oligonucleotide, double  
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
 CC to treat conditions such as Alzheimer's disease. The agent can be used as  
 CC an APP pathway modulator or in gene therapy. This polynucleotide sequence  
 CC represents the DNA of the APP related human homologue hCP35211.

XX Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;

XX Query Match 94.6%; Score 193; DB 24; Length 2404;

XX Best Local Similarity 99.5%; Pred. No. 4.1e-55;

XX Matches 204; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTGAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60  
 Db 520 GAAGAAGCTAGATTAAAGTCCTTTGAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 579  
 QY 61 GAGTTAGCAAGTCTGGACTCTACTACAGAGTATTGGTGACCAAGTGCAGTCTTTTGT 120  
 Db 580 GAGTTAGCAAGTCTGGACTCTACTACAGAGTATTGGTGACCAAGTGCAGTCTTTTGT 639  
 QY 121 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGCTGATCAGAACACAGCGG 179  
 Db 640 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGCTGATCAGAACACAGCGG 699  
 QY 180 ACACCTTTCCTAATTTGCTTTCTTTT 204  
 Db 700 ACACCTTTCCTAATTTGCTTTCTTTT 724

## RESULT 8

AAAT70839

ID AAT70839 standard; cDNA; 2100 BP.

XX AAT70839;

XX 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor m-xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
 KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
 KW Ischaemia; myocardial infarction; stroke;  
 KW reperfusion injury; toxin-induced liver disease; gene therapy;  
 KW diagnosis; ds.

XX Mus sp.

XX Key Location/Qualifiers

FT 127..1617

FT /\*tag= a

XX WO9706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.

XX 04-AUG-1995; 95US-0511485.

XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;

XX WPI; 1997-154262/14.

XX P-PSDB; AAM19584.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients; and for detection  
 PT of susceptibility to apoptotic disease

XX Claim 11; Page 78-79; 219pp; English.

XX Human xiap, hlap-1 and hlap-2 genes, and murine xiap, hlap-1 and  
 CC hlap-2 genes (AA70836-41) respectively code for a new class of  
 CC mammalian proteins (AAM19581-86) that are inhibitors of apoptosis  
 CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was  
 CC constructed from 12 overlapping clones isolated from a mouse  
 CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic  
 CC library using human xiap cDNA as probe. IAP nucleic acids can be  
 CC used to express IAP polypeptides in cells and animals to inhibit  
 CC apoptosis, and as primers and probes to identify and isolate  
 CC additional IAP genes, as well as in methods for treating diseases  
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).

XX SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;  
Query Match 84.3%; Score 172; DB 18; Length 2100;  
Best Local Similarity 90.2%; Pred. No. 5.1e-48;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCAGCTAACCCCAAGA 60  
DB 613 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGACTATGCTCATTATACCCCCAGA 672  
QY 61 GATTTAGCAAGTCGCTGAGCTCTACTACACAGGATTTGGTGCAGTGCAGTCTTTTGT 120  
DB 673 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 732  
QY 121 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATCGTGCCTGCTGCAGAACACAGGCGA 180  
DB 733 TGTGGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGCCTGCTGCAGAACACAGGAGA 792  
QY 181 CACTTTCCTAATGCTCTTTTGT 204  
DB 793 CACTTTCCTAATGCTCTTTTGT 816  
RESULT 9  
ID ABK93872 standard; cDNA; 2100 BP.  
XX AC ABK93872;  
XX DT 26-AUG-2002 (first entry)  
XX DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.  
XX KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX OS Mus sp.  
XX PN WO200226968-A2.  
XX PD 04-APR-2002.  
XX PF 27-SEP-2001; 2001WO-CA01379.  
XX PR 28-SEP-2000; 2000US-0672717.  
XX PA (UYOT-) UNIV OTTAWA.  
XX PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX WPI; 2002-479562/51.  
XX DR P-PSDB; ABG65666.  
XX PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
PT enhancing apoptosis in a cell, for treating cancer and other  
PT proliferative diseases  
XX PS Disclosure; Fig 4; 135pp; English.  
XX CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
CC length of the antisense nucleic acid, the IAP proteins may be mouse  
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
CC composition comprising a mammalian IAP antisense molecule and a method of  
CC enhancing apoptosis in a cell, comprising administering a negative  
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a

CC mammal diagnosed with a proliferative disease. The method is useful for  
CC treating a patient diagnosed with a proliferative disease like cancer.  
CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
CC conditions where apoptosis is involved or implicated (e.g. embryonic  
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP  
CC cDNA sequence.  
XX SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;  
Query Match 84.3%; Score 172; DB 24; Length 2100;  
Best Local Similarity 90.2%; Pred. No. 5.1e-48;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCAGCTAACCCCAAGA 60  
DB 613 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGACTATGCTCATTATACCCCCAGA 672  
QY 61 GAGTTAGCAAGTCGCTGAGCTCTACTACACAGGATTTGGTGCAGTGCAGTCTTTTGT 120  
DB 673 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 732  
QY 121 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATCGTGCCTGCTGCAGAACACAGGCGA 180  
DB 733 TGTGGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGCCTGCTGCAGAACACAGGAGA 792  
QY 181 CACTTTCCTAATGCTCTTTTGT 204  
DB 793 CACTTTCCTAATGCTCTTTTGT 816  
RESULT 10  
ID AAV55041 standard; cDNA; 2691 BP.  
XX AC AAV55041;  
XX DT 13-NOV-1998 (first entry)  
XX DE Murine XIAP coding sequence.  
XX KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.  
XX OS Mus sp.  
XX PH Key Location/Qualifiers  
XX CDS 572...2162  
XX FT /\*tag= a  
XX FT /product= XIAP  
XX PN WO9835693-A2.  
XX PD 20-AUG-1998.  
XX PF 13-FEB-1998; 98WO-IB00781.  
XX PR 13-FEB-1997; 97US-0800929.  
XX PA (UYOT-) UNIV OTTAWA.  
XX PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
XX TSang B;  
XX DR WPI; 1998-467164/40.  
XX DR P-PSDB; AAW69297.  
XX PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
PT of IAP or NAIP polypeptide - also methods for prognosis based on  
PT presence of IAP and NAIP, specifically applied to cancers involving

p53 mutations

XX.  
XX.  
PS  
PS  
Claim 13; Fig 4; 147pp; English.

This sequence encodes the mouse XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver, esopharynx, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.

XX.  
SQ Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;

Query Match 84.3%; Score 172; DB 19; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 5.7e-48;  
Matches 164; Conservative 0; Mismatches 20; Indels 0; Gaps 0

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACATGGCCAGACTATGCTCAGCTAACCCCAAGA 60  
|||||  
Db 1158 GAGAAGCCAGATTGAAGTCATTTTCAGAACATGGCCGAGCTATGCTCATTTAACCOCAG 1217

QY 61 GAGTTAGCAAGTGCTGGACTCTACTACACAGGTATTTGTTGACCAAGTCGAGTGCCTTTGT 120  
|||||  
Db 1218 GAGTTAGCTAGTGTGCCCTCTACTACAGAGGGGTGATGATCAAGTGCATTCGCTTTGT 1277

QY 121 TGTGGTGGAAAACGAAAAATTGGGAACCTTTGTGATCGTCTGCTGGTCAGAACACAGGCCGA 180  
|||||  
Db 1278 TGTGGGGGAAAACGAAAAATTGGGAACCCCTGTGATCGTCTGCTGGTCAGAACACAGGAGA 1337

QY 181 CACTTTCCTTAATTCCTTTCTTTGTT 204  
|||||  
Db 1338 CACTTTCCCAATTGCTTTTTTTGTT 1361

RESULT 11	
AAAT72710	
ID	AAAT72710 standard; DNA; 1988 BP.
XX	
XX	
XX	AAAT72710;
XX	
XX	16-SEP-1997 (first entry)
XX	
XX	Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX	
KW	Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
KW	degenerative disease; infectious disease; autoimmune disease;
KW	cancer; gene therapy; diagnosis; ss.
XX	
XX	
OS	Mus musculus.
XX	
FH	Key
FT	Location/Qualifiers
FT	212..1702
FT	/*tag= a
XX	
XX	
PN	W09723501-A1.
XX	
XX	
PD	03-JUL-1997.
XX	
PF	20-DEC-1996; 96WO-AU00827.
XX	
PR	22-DEC-1995; 95AU-0007275.
XX	
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.
XX	

PI	Vaux DL;
XX	
DR	WPI; 1997-350966/32.
DR	P-PSDB; AAW19745.
XX	
PT	Isolated protein homologues of viral inhibitors of apoptosis - used
PT	to modulate apoptosis for treatment of degenerative, infectious or
PT	autoimmune diseases and cancer
XX	
XX	Claim 24; Page 44-47; 136pp; English.
XX	
CC	An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
CC	homologue A (MHA) (AAW19745), a murine homologue of baculovirus
CC	inhibitor of apoptosis protein (IAP). It was isolated from a mouse
CC	liver cDNA library on the basis of homology to Orgyia pseudotaugata
CC	polyhedrosis virus IAP BIR and RING finger amino acid motifs.
CC	Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
CC	to produce polypeptides useful in methods for modulating apoptosis
CC	in animal cells, specifically for treatment, by inhibition, of
CC	degenerative and infectious disease or, by promotion, of cancer and
CC	autoimmune disease, and can be used for gene therapy of these
CC	diseases.
XX	
SQ	Sequence 1988 BP; 505 A; 367 C; 459 G; 557 T; 0 other;
	Query Match            83.5%; Score 170.4; DB 18; Length 1988;
	Best Local Similarity 89.7%; Pred. No. 1.8e-47;
	Matches 183; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY	1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCGCAGACTGCTCACCTAACCCCAAGA 60
DB	698 GAAGAAGCCGAATGAAGTCAATTCAGAACTGGCGGACTATGTCTCAATTACCCCCAGA 757
QY	61 GAGTTAGCAAGTGCTGGACTCTACTACACAGGTATTGGTGACCAGTGCAGTGTCTTTGT 120
DB	758 GAGTTAGTAGTGCTGGCCCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTGT 817
QY	121 TGCTGGTGGAAAACGTAAAAATTTGGGAACCTTTGTGATCGTGCCTGCTCAGAACACAGGCGA 180
DB	818 TGTGGGGAAAACGTGAAAAATTTGGGAACCCCTGTGATCGTGCCTGCTCAGAACACAGGAGA 877
QY	181 CACTTTCTTAATGCTCTTTTGT 204
DB	878 CACTTTCCAATGCTTTTGT 901
	RESULT 12
ID	ABK14677
XX	ABK14677 standard; cDNA; 1758 BP.
XX	ABK14677;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA.
XX	
KW	Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;
KW	antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;
KW	chromosome 19; vaccine; gene therapy; hyperproliferative disease;
KW	cancer; transgenic animal; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	CDS 286..1680
FT	/*tag= a
FT	/product= "IAPL7 protein"
FT	/partial
ET	/note= "No start codon shown"
XX	
FN	WO2000210391-A1.
XX	
PD	07-FEB-2002.

XX 18-JUL-2001; 2001WO-EP08287.  
PF  
XX 28-JUL-2000; 2000EP-0116452.  
PR  
XX (MERE ) MERCK PATENT GMBH.  
PA  
XX Hentsch B;  
PI  
XX WPI: 2002-188741/24.  
DR  
DR P-PSDB; AAU75747.  
XX  
XX New inhibitor of apoptosis proteins and polynucleotides useful in  
PT vaccines for inducing an immune response against hyperproliferative  
PT diseases e.g. cancer  
XX  
XX Claim 5; Page 33-35; 41pp; English.  
PS  
XX This invention relates to the nucleic acid and protein sequences of a  
CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences  
CC have homology to the IAP (inhibitors of apoptosis) gene family which  
CC are thought to inhibit proteins by regulating the anti-apoptotic  
CC activity of the V-Rel and NF-kappaB family of transcription factors.  
CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids  
CC of the invention are useful for screening to identify compounds that  
CC stimulate or inhibit the function or level of IAPL7, where the  
CC identified compounds are useful for treating hyper-proliferative  
CC diseases such as cancer. The protein sequences may also be used to  
CC identify membrane bound or soluble receptors of IAPL7 by standard  
CC receptor binding techniques. Nucleic acids encoding IAPL7, may be used  
CC as hybridisation probes for cDNA and genomic DNA, or as primers for  
CC nucleic acid amplification reaction and the primers and probes may also  
CC be used to isolate full-length cDNAs and genomic clones encoding IAPL7.  
CC The nucleic acid sequences are useful as diagnostic reagents for  
CC diagnosing a disease or a susceptibility to a disease by detecting  
CC mutations in the associated gene. The nucleic acid sequence is useful  
CC for chromosome localisation and tissue expression studies and is also  
CC useful for producing transgenic animals. The IAPL7 protein sequence may  
CC also be used to generate an anti-IAPL7 antibody which is useful in  
CC screening methods for detecting the effect of added compounds on the  
CC production of mRNA and protein in cells. The sequences of the invention  
CC are also useful as vaccines for inducing an immunological response in a  
CC mammal. The present sequence represents the cDNA encoding the human  
CC inhibitor of apoptosis 7 (IAP7) protein of the invention.  
XX  
SQ Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;  
Query Match 81.2%; Score 165.6; DB 24; Length 1758;  
Best Local Similarity 88.2%; Pred. No. 7, 1e-46;  
Matches 180; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACACTAACCCCAAGA 50  
DB 673 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACACTAACCCCAAGA 732  
QY 61 GAGTTAGCAAGTCGTGACTCTACTACACAGGTATTGGTACACAGTGCAGTCTTCT 120  
DB 733 GAGCTGGCCAGTCTGGCTGTACTACACAGGCACTGATCAGGTCAGTCTCTGT 792  
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTCTGGTGTGCAACACAGGCGA 180  
DB 793 TGTGGCGGAAACTGAAAACTGGAACTGTGATCGTCTGGTGTGCAACACAGGCGA 852  
QY 181 CACTTCTCTAATGCTCTTTTGT 204  
DB 853 CATTTCCTTAATGCTCTTTTATT 876  
RESULT 13  
ABK13197  
ID ABK13197 standard; DNA; 1559 BP.  
XX  
AC ABK13197;

XX 23-APR-2002 (first entry)  
DT  
XX Human testes specific inhibitor of apoptosis (TIAP) gene.  
DE  
XX TIAP; apoptosis; testes specific inhibitor of apoptosis; gene;  
KW human; ds; apoptotic; cytostatic; anti-infertility; contraceptive;  
KW chromosome 12q22-23; transgenic animal; antibody; immunogen;  
KW testicular cell; testicular cancer; cancer; male infertility;  
KW male birth control; XIAP.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT CDS 791..1501  
FT /\*tag= a  
FT /product= "TIAP protein"  
XX  
XX US6331412-B1.  
PN  
XX 18-DEC-2001.  
PD  
XX 29-JAN-1999; 98US-0239867.  
PF  
XX 29-JAN-1998; 98US-073001P.  
PR  
XX (UWOT-) UNIV OTTAWA.  
PA  
XX Korneluk RG, Lagace M;  
PI  
XX WPI: 2002-105275/14.  
DR  
XX P-PSDB; AAU75066.  
XX  
PT Nucleic acids encoding a testis specific apoptosis inhibitor protein  
PT (TIAP) useful for treating testicular cancers, cancers in  
PT non-testicular tissues, male infertility, and for achieving male birth  
PT control  
XX  
XX Claim 2; Fig 4A; 29pp; English.  
XX  
XX This invention relates to a novel isolated nucleic acid molecule  
CC encoding a TIAP polypeptide (testes-specific inhibitor of apoptosis)  
CC protein. This gene is a homologue of the X-linked XIAP gene and is  
CC located on chromosome 12q22-23. The nucleotide and protein sequences of  
CC the invention and vectors containing these sequences may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate TIAP expression. Additionally, the nucleotide sequence may  
CC be used to express the TIAP protein by recombinant methods. Conversely,  
CC antisense nucleic acid molecules may be administered to down-regulate  
CC TIAP expression. The nucleotide sequence, may also be used to design DNA  
CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to  
CC detect and quantitate the presence of similar nucleic acid sequences in  
CC samples, to identify patients who may be in need of restorative therapy.  
CC Through the production of transgenic animals and cells, the sequences  
CC may also be used to study the expression and function of TIAP proteins  
CC and their role in metabolism. The TIAP polypeptides may be used to  
CC produce antibodies against TIAP and may be used to identify modulators  
CC (agonists and antagonists) of TIAP expression and activity. An anti-TIAP  
CC antibody or antagonist may also be used to down-regulate TIAP expression  
CC and activity. The reagents may be used in this way for the treatment of  
CC excessive or insufficient apoptosis, particularly in testicular cells.  
CC In particular they are useful in diagnosing and treating testicular  
CC cancers, cancers in non-testicular tissues, male infertility, and for  
CC achieving male birth control. The present sequence represents the  
CC human TIAP gene sequence of the invention.  
XX  
SQ Sequence 1559 BP; 465 A; 309 C; 396 G; 387 T; 2 other; 1

Query Match 80.4%; Score 164; DB 24; Length 1559;  
Best Local Similarity 87.7%; Pred. No. 2, 4e-45;  
Matches 179; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACACTAACCCCAAGA 60

|||||  
 494 GAAGAGCTAGATACAGTCGTTTCAACTGGCCAGCCTCTGCCACATTGACCCCGAGA 553  
 61 GAGTTAGCAAGTCGTGGAGCTCTACTACACAGGTATTGGTACCAAGTCAGTGGCTTTTGT 120  
 554 GAGCTGGCCAGTCGTGGCTGTACTACACAGGCACTGATGACCAAGTCAGTGGCTTCTGT 613  
 121 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGGTCAGAACACAGCGGA 180  
 614 TGTGGCGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGGTCAGAACACAGCGGA 673  
 181 CACTTTCCTAAATGCTCTTTTGT 204  
 674 CATTTTCCTAAATGCTCTTTTATT 697

RESULT 14  
 ABK14678  
 ID ABK14678 standard; cDNA; 1758 BP.  
 XX  
 AC ABK14678;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA #2.  
 XX  
 KW Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;  
 KW antiapoptotic; IAP; apoptosis; V-Rel; NF-kappaB; antibody;  
 KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;  
 KW cancer; transgenic animal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 286..687  
 FT /\*tag= a  
 FT /product= "IAPL7 protein"  
 FT /partial  
 FT /note= "This sequence encodes amino acid  
 residues 1-133 of the protein shown in  
 AAU75747. NO start codon shown"  
 FT  
 XX  
 PN WO200210381-A1.  
 XX  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 18-JUL-2001; 2001WO-EP08287.  
 XX  
 XX 28-JUL-2000; 2000EP-0116452.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Hentsch B;  
 XX  
 XX WPI; 2002-188741/24.  
 XX  
 PT New inhibitor of apoptosis proteins and polynucleotides useful in  
 PT vaccines for inducing an immune response against hyperproliferative  
 PT diseases e.g. cancer  
 XX  
 XX  
 PS Claim 5; Page 36-38; 41pp; English.  
 XX  
 CC This invention relates to the nucleic acid and protein sequences of a  
 CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences  
 CC have homology to the IAP (inhibitors of apoptosis) gene family which  
 CC are thought to inhibit proteins by regulating the anti-apoptotic  
 CC activity of the V-Rel and NF-kappaB family of transcription factors.  
 CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids  
 CC of the invention are useful for screening to identify compounds that  
 CC stimulate or inhibit the function or level of IAPL7, where the  
 CC identified compounds are useful for treating hyper-proliferative  
 CC diseases such as cancer. The protein sequences may also be used to  
 CC identify membrane bound or soluble receptors of IAPL7 by standard

receptor binding techniques. Nucleic acids encoding IAPL7, may be used  
 as hybridisation probes for cDNA and genomic DNA, or as primers for  
 nucleic acid amplification reaction and the primers and probes may also  
 be used to isolate full-length cDNAs and genomic clones encoding IAPL7.  
 The nucleic acid sequences are useful as diagnostic reagents for  
 diagnosing a disease or a susceptibility to a disease by detecting  
 mutations in the associated gene. The nucleic acid sequence is useful  
 for chromosome localisation and tissue expression studies and is also  
 useful for producing transgenic animals. The IAPL7 protein sequence may  
 also be used to generate an anti-IAPL7 antibody which is useful in  
 screening methods for detecting the effect of added compounds on the  
 production of mRNA and protein in cells. The sequences of the invention  
 are also useful as vaccines for inducing an immunological response in a  
 mammal. The present sequence represents the human inhibitor of apoptosis  
 7 (IAP7) cDNA #2 of the invention. This sequence is the same as the  
 sequence shown in ABK14677 but has a stop codon at nucleotides 685-687.  
 XX  
 SQ Sequence 1758 BP; 489 A; 371 C; 470 G; 428 T; 0 other;  
 Query Match 80.4%; Score 164; DB 24; Length 1758;  
 Best Local Similarity 87.7%; Pred. NO. 2.5e-45;  
 Matches 179; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGCTATCTCTACCTAACCCCAAGA 60  
 DB 673 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGCTCTCTGACCTTGACCCCGAGA 732  
 QY 61 GAGTTAGCAAGTCGTGGAGCTCTACTACACAGGTATTGGTACCAAGTCAGTGGCTTTTGT 120  
 DB 733 GAGCTGGCCAGTCGTGGCTGTACTACACAGGCACTGATGACCAAGTCAGTGGCTTCTGT 792  
 QY 121 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGGTCAGAACACAGCGGA 180  
 DB 793 TGTGGCGGAAACTGAAATTTGGGAACCTTGTGATCGTGGCTGGTCAGAACACAGCGGA 852  
 QY 181 CACTTTCCTAAATGCTCTTTTGT 204  
 DB 853 CATTTTCCTAAATGCTCTTTTATT 876

RESULT 15  
 AAD03581  
 ID AAD03581 standard; cDNA; 4993 BP.  
 XX  
 AC AAD03581;  
 XX  
 DT 19-JUN-2001 (first entry)  
 XX  
 DE Human IAP-like protein-2 (ILP-2) cDNA.  
 XX  
 KW Human; inhibitor of apoptosis; IAP-like protein-2; ILP-2;  
 KW chromosome 19q13.3-q13.4; transforming growth factor beta receptor;  
 KW TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;  
 KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;  
 KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;  
 KW retinal degeneration; hyperferritinemia-cataract syndrome; cancer;  
 KW autoimmune disease; diabetes; multiple sclerosis; cytostatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 2074..2784  
 FT /\*tag= a  
 FT /product= "Human inhibitor of apoptosis (IAP)-like  
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 FT  
 XX  
 XX WO200123568-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 XX 29-SEP-2000; 2000WO-US26735.  
 XX  
 XX 30-SEP-1999; 99US-0157169.  
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	204	100.0	1588	4	US-09-239-867-3
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3	204	100.0	2540	3	US-09-392-580-1
4	204	100.0	5232	3	US-09-212-971-3
5	204	100.0	5232	3	US-08-800-929A-3
6	204	100.0	5232	4	US-09-617-053A-3
7	172	84.3	2100	2	US-08-511-485-9
8	172	84.3	2691	3	US-09-212-971-9
9	172	84.3	2691	3	US-08-800-929A-9
10	172	84.3	2691	4	US-09-617-053A-9
11	164	80.4	1559	4	US-09-239-867-1
12	84.6	41.5	2601	4	US-08-569-749-3
13	84.6	41.5	2601	5	PT-08-596-12860-3
14	84.6	41.5	2676	2	US-08-511-485-5
15	84.6	41.5	3076	2	US-09-205-144-1
16	84.6	41.5	6669	3	US-09-212-971-5
17	84.6	41.5	6669	3	US-08-800-929A-5
18	84.6	41.5	6669	4	US-09-617-053A-5
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31 68.6 33.6 1435 5 PCT-US95-05922A-1  
32 62.8 30.8 2676 3 US-09-212-971-11  
33 62.8 30.8 2676 3 US-08-800-929A-11  
34 62.8 30.8 2676 4 US-09-617-053A-11  
35 58.2 28.5 5502 3 US-08-836-134-1  
36 58.2 28.5 5502 4 US-09-493-784-1  
37 41.2 20.2 711 3 US-09-121-979-3  
38 41.2 20.2 711 4 US-09-332-319-3  
39 38.8 19.0 176373 3 US-09-128-155-17  
C 40 38.4 18.8 152331 3 US-09-128-155-16  
C 41 28 13.7 28 2 US-08-859-998-1232  
C 42 28 13.7 28 4 US-09-225-928-1232  
C 43 28 13.7 1287 4 US-09-028-274A-16  
C 44 27.8 13.6 2000 4 US-09-553-889A-1  
C 45 27.6 13.5 758 4 US-09-712-016-28

## ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-239-867-3

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Best Local Similarity 100.0%; Pred No. 8.6e-62;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
Db 520 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579  
QY 61 GAGTTAGCAAGTCTGCGACTCTACTACAGAGTATTTGGTACCAAGTGCAGTCTTTGT 120  
|||||  
Db 580 GAGTTAGCAAGTCTGCGACTCTACTACAGAGTATTTGGTACCAAGTGCAGTCTTTGT 639  
QY 121 TGTGGTGGAACTGAAATTTGGGAACCTTGTGATCGTCGCTGTCAGAACACAGCGGA 180  
|||||  
Db 640 TGTGGTGGAACTGAAATTTGGGAACCTTGTGATCGTCGCTGTCAGAACACAGCGGA 699  
QY 181 CACTTTCCTAATTCCTTTTGT 204  
|||||  
Db 700 CACTTTCCTAATTCCTTTTGT 723

RESULT 2  
US-08-511-485-3  
; Sequence 3, Application US/08511485  
; Patent No. 5919912  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen



;; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
;; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
;; NUMBER OF SEQUENCES: 38  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/511,485  
;; FILING DATE: 04-AUG-1995  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 07540/002001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617/542-5070  
;; TELEFAX: 617/542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2540 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: DNA (genomic)  
US-08-511-485-3

Query Match 100.0%; Score 204; DB 2; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 1e-61;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60  
|||||  
DB 520 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579  
QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120  
|||||  
DB 580 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 639  
QY 121 TGTGGTGAAGAACTGAAATAATTGGGAACCTTGTGATCGCTGGTCAGACACAGGCGA 180  
|||||  
DB 640 TGTGGTGAAGAACTGAAATAATTGGGAACCTTGTGATCGCTGGTCAGACACAGGCGA 699  
QY 181 CACTTCTCTAATTCCTCTTTGTT 204  
|||||  
DB 700 CACTTCTCTAATTCCTCTTTGTT 723

RESULT 3  
US-09-392-580-1  
; Sequence 1, Application US/09392580  
; Patent No. 6087173  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIO  
; FILE REFERENCE: RFS-0072  
; CURRENT APPLICATION NUMBER: US/09/392,580  
; CURRENT FILING DATE: 1999-09-09  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 2540  
; TYPE: DNA

;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (34)..(1527)  
US-09-392-580-1

Query Match 100.0%; Score 204; DB 3; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 1e-61;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60  
|||||  
DB 520 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579  
QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120  
|||||  
DB 580 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 639  
QY 121 TGTGGTGAAGAACTGAAATAATTGGGAACCTTGTGATCGCTGGTCAGACACAGGCGA 180  
|||||  
DB 640 TGTGGTGAAGAACTGAAATAATTGGGAACCTTGTGATCGCTGGTCAGACACAGGCGA 699  
QY 181 CACTTCTCTAATTCCTCTTTGTT 204  
|||||  
DB 700 CACTTCTCTAATTCCTCTTTGTT 723

RESULT 4  
US-09-212-971-3  
; Sequence 3, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; CURRENT FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5232  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4623)..(4623)  
; OTHER INFORMATION: n can be any nucleotide  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4622)..(4622)  
; OTHER INFORMATION: n can be any nucleotide  
US-09-212-971-3

Query Match 100.0%; Score 204; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 1e-61;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60  
|||||  
DB 520 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579

QY 61 GAGTACCAAGTCTGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120  
|||||  
Db 580 GAGTACCAAGTCTGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 639  
|||||  
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGTCGCTGGTGACCAAGTGCAGTCTTTGT 180  
|||||  
Db 640 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGTCGCTGGTGACCAAGTGCAGTCTTTGT 699  
|||||  
QY 181 CACTTTCCTAATGCTCTTTGTT 204  
|||||  
Db 700 CACTTTCCTAATGCTCTTTGTT 723  
|||||

## RESULT 5

US-08-800-929A-3  
; Sequence 3, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,929A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,590  
; FILING DATE: 14-NOV-1996  
; APPLICATION NUMBER: 60/017,354  
; FILING DATE: 26-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bleker-Brady, Kristina  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 07891/009001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5232 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1..5232  
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

Query Match 100.0%; Score 204; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAAACCCCAAGA 60  
|||||  
Db 520 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAAACCCCAAGA 579  
|||||  
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120  
|||||  
Db 580 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 639  
|||||  
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGTCGCTGGTGACCAAGTGCAGTCTTTGT 180  
|||||  
Db 640 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGTCGCTGGTGACCAAGTGCAGTCTTTGT 699  
|||||  
QY 181 CACTTTCCTAATGCTCTTTGTT 204  
|||||  
Db 700 CACTTTCCTAATGCTCTTTGTT 723  
|||||

## RESULT 6

US-09-617-053A-3  
; Sequence 3, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009003  
; CURRENT APPLICATION NUMBER: US/09/617,053A  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5232  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4623)...(4623)  
; OTHER INFORMATION: n can be any nucleotide  
; NAME/KEY: variation  
; LOCATION: (4622)...(4622)  
; OTHER INFORMATION: n can be any nucleotide  
; US-09-617-053A-3

Query Match 100.0%; Score 204; DB 4; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 1.4e-61;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAAACCCCAAGA 60  
|||||  
Db 520 GAAGAAGCTAGATTAAAGTCTCTTTTCAGAACTGGCCAGACTATGCTACCTAAACCCCAAGA 579  
|||||  
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120  
|||||  
Db 580 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 639  
|||||  
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGTCGCTGGTGACCAAGTGCAGTCTTTGT 180  
|||||  
Db 640 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGTCGCTGGTGACCAAGTGCAGTCTTTGT 699  
|||||  
QY 181 CACTTTCCTAATGCTCTTTGTT 204  
|||||  
Db 700 CACTTTCCTAATGCTCTTTGTT 723  
|||||

```
RESULT 7
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match      84.3%; Score 172; DB 2; Length 2100;
Best Local Similarity 90.2%; Pred. No. 1.5e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCAGCTTAACCCCAAGA 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 613 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 672
QY 61 GAGTTAGCAAGTGGGACTCTACTACACAGTATTTGGTGACCAAGTGCAGTGCTTTTGT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 673 GAGTTAGTCTAGTGGCTCTACTACACAGGGGCTGATCAAGTCAATGCTTTTGT 732
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTTGTATCGTCTGCTGCTCAGAACACAGGCGA 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 733 TGTGGGGGAAACTGAAATTTGGAACTTTGTATCGTCTGCTGCTCAGAACACAGGAGA 792
QY 181 CACTTTCCTAATTGCTTTTGT 204
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 793 CACTTTCCTAATTGCTTTTGT 816

RESULT 8
US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
```

```
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

Query Match      84.3%; Score 172; DB 3; Length 2691;
Best Local Similarity 90.2%; Pred. No. 1.6e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCAGCTTAACCCCAAGA 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 1217
QY 61 GAGTTAGCAAGTGGGACTCTACTACACAGTATTTGGTGACCAAGTGCAGTGCTTTTGT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1218 GAGTTAGTCTAGTGGCTCTACTACACAGGGGCTGATCAAGTCAATGCTTTTGT 1277
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTTGTATCGTCTGCTGCTCAGAACACAGGCGA 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1278 TGTGGGGGAAACTGAAATTTGGAACTTTGTATCGTCTGCTGCTCAGAACACAGGAGA 1337
QY 181 CACTTTCCTAATTGCTTTTGT 204
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1338 CACTTTCCTAATTGCTTTTGT 1361

RESULT 9
US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2691 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-800-929A-9

Query Match 84.3%; Score 172; DB 3; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 1.6e-50;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60  
DB 1158 GAAGAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 1217  
QY 61 GAGTTAGCAAGTGTGGGCTCTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 1218 GAGTTAGTGTGGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 1277  
QY 121 TGTGGTGAAGTGTGGGCTCTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 1278 TGTGGGGAAGTGTGGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 1277  
QY 121 TGTGGTGAAGTGTGGGCTCTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 1278 TGTGGGGAAGTGTGGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 1277  
QY 181 CACTTTCCTAATTGCTTCTTTTGT 204  
DB 1338 CACTTTCCTAATTGCTTCTTTTGT 1361

RESULT 10  
US-09-617-053A-9  
Sequence 9, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 2691  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-617-053A-9

Query Match 84.3%; Score 172; DB 4; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 1.6e-50;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60  
DB 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 1217  
QY 61 GAGTTAGCAAGTGTGGGCTCTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 1218 GAGTTAGTGTGGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 1277  
QY 121 TGTGGTGAAGTGTGGGCTCTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 1278 TGTGGGGAAGTGTGGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 1277  
QY 181 CACTTTCCTAATTGCTTCTTTTGT 204  
DB 1338 CACTTTCCTAATTGCTTCTTTTGT 1361

RESULT 11  
US-09-239-867-1  
Sequence 1, Application US/09239867  
Patent No. 6331412  
GENERAL INFORMATION:  
APPLICANT: Robert G. Korneluk et al.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
TITLE OF INVENTION: MALE FERTILITY  
FILE REFERENCE: 07891/018002  
CURRENT APPLICATION NUMBER: US/09/239,867  
CURRENT FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/073,001  
PRIOR FILING DATE: 1998-01-29  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1559  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1559)  
OTHER INFORMATION: n = A,T,C or G  
US-09-239-867-1

Query Match 80.4%; Score 164; DB 4; Length 1559;  
Best Local Similarity 87.7%; Pred. No. 8.1e-48;  
Matches 179; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60  
DB 494 GAAGAAGCTAGATAACAGTCGTTTCACAACTGGCCGAGCTTGGCCCACTGACCCCGAGA 553  
QY 61 GAGTTAGCAAGTGTGGGCTCTACTACACAGGTTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 554 GAGCTGGCCAGTGTGGGCTGTACTACAGGCTGATGATCAAGTGCATGCTTTTGT 613  
QY 121 TGTGGTGAAGTGTGGGCTCTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120  
DB 614 TGTGGGGAAGTGTGGGCTCTACTACAGGCTGATGATCAAGTGCATGCTTTTGT 613  
QY 181 CACTTTCCTAATTGCTTCTTTTGT 204  
DB 674 CACTTTCCTAATTGCTTCTTTTGT 697

RESULT 12  
US-08-569-749-3  
Sequence 3, Application US/08569749  
Patent No. 6187557  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike



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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
; US-08-511-485-5
;
; Query Match 41.5%; Score 84.6; DB 2; Length 2676;
; Best Local Similarity 67.0%; Pred. No. 5.7e-20;
; Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
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; QY 1 GAAGAAGCTAGATTAAAGTCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
; DB 693 GAAATGCCAGATTACTTCTTTCAGACATGGCCA---TTGACTTTTCTGTCGCCAACA 749
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; QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120
; DB 750 GATCTGSCACGAGCGGCTTTTACTATAGGACCTGGAGACAGAGTGGCTTGTGCTGCC 809
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; QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGCTGCTGGTCAGAACACAGGCGA 180
; DB 810 TGTGGTGGAAATTTGACCAATTTGGAACTGGAAGCAAGTATGCTATGTCAGAACACCTGAGA 869
;
; QY 181 CACTTTCTCTAAATGCTCTTTGT 203
; DB 870 CATTTCCTCAATGCCCATTTAT 892
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; RESULT 15
; US-09-205-144-1
; Sequence 1, Application US/09205144
; Patent No. 5958771
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRES
; FILE REFERENCE: RTS-0021
; CURRENT APPLICATION NUMBER: US/09/205,144
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (725)..(2539)
; US-09-205-144-1
;
; Query Match 41.5%; Score 84.6; DB 2; Length 3076;
; Best Local Similarity 67.0%; Pred. No. 5e-20;
; Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
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; QY 1 GAAGAAGCTAGATTAAAGTCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
; DB 1229 GAAATGCCAGATTACTTCTTTCAGACATGGCCA---TTGACTTTTCTGTCGCCAACA 1285
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; QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120
; DB 1286 GATCTGSCAAGCAGGCTTTTACTATAGGACCTGGAGACAGAGTGGCTTGTGCTGCC 1345
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; QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATGCTGCTGGTCAGAACACAGGCGA 180
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QY 181 CACTTTCTCTAAATGCTCTTTGT 203
DB 1406 CATTTCCTCAATGCCCATTTAT 1428

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 49.0521 Seconds

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Perfect score: 204

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Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186058

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	204	100.0	2540	9	US-09-201-936-3	Sequence 3, Appl1
2	204	100.0	5232	10	US-09-974-592-3	Sequence 3, Appl1
3	193	94.6	2404	9	US-09-964-899-38	Sequence 38, Appl1
4	172	84.3	2100	9	US-09-201-936-9	Sequence 9, Appl1
5	172	84.3	2691	10	US-09-974-592-9	Sequence 9, Appl1
6	84.6	41.5	2676	9	US-09-201-936-5	Sequence 5, Appl1
7	84.6	41.5	3076	9	US-09-954-531-16	Sequence 16, Appl1
8	84.6	41.5	6669	10	US-09-934-456-1635	Sequence 1635, Ap
9	84.6	41.5	6669	10	US-09-974-592-5	Sequence 5, Appl1
10	78.4	38.4	240	9	US-09-796-692-3493	Sequence 3493, Ap
11	76.8	37.6	240	9	US-09-796-692-6687	Sequence 6687, Ap
12	74.4	36.5	3151	10	US-09-974-592-13	Sequence 13, Appl1
13	72.8	35.7	2416	9	US-09-201-936-41	Sequence 41, Appl1
14	70.2	34.4	2291	10	US-09-778-927A-21	Sequence 21, Appl1
15	70.2	34.4	2580	9	US-09-201-936-7	Sequence 7, Appl1
16	70.2	34.4	3532	10	US-09-880-107-3354	Sequence 3354, Ap
17	70.2	34.4	3732	10	US-09-974-592-7	Sequence 7, Appl1
18	62.8	30.8	2450	9	US-09-201-936-39	Sequence 39, Appl1
19	62.8	30.8	2676	10	US-09-974-592-11	Sequence 11, Appl1

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20 59.8 29.3 6124 8 US-08-913-322-21
21 59.8 29.3 6124 10 US-09-967-768A-184
22 59.8 29.3 6133 8 US-08-913-322-2
23 59.8 29.3 6228 8 US-08-913-322-23
24 58.2 28.5 5504 8 US-08-913-322-1
25 54.2 26.6 3773 9 US-10-041-859-1
26 38.8 19.0 176373 9 US-10-095-407-17
27 38.4 18.8 152331 9 US-10-095-407-16
28 29.8 14.6 299 10 US-09-878-574-13884
29 29.4 14.4 420 10 US-09-960-352-14727
30 29 14.2 396 10 US-09-864-761-26657
31 29 14.2 477 10 US-09-864-761-10014
32 28.6 14.0 471 10 US-09-864-761-5515
33 28 13.7 1304 9 US-10-108-383-1
34 28 13.7 1559 10 US-09-867-550-1503
35 28 13.7 1656 9 US-10-028-072-239
36 28 13.7 1656 9 US-10-121-049-239
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38 28 13.7 1656 9 US-10-140-470-239
39 28 13.7 1656 9 US-10-175-746-239
40 28 13.7 1656 9 US-10-176-918-239
41 28 13.7 1656 9 US-10-176-921-239
42 28 13.7 1656 9 US-10-137-865-239
43 28 13.7 1656 9 US-10-140-474-239
44 28 13.7 1656 9 US-10-142-431-239
45 28 13.7 1656 9 US-10-143-114-239

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#### ALIGNMENTS

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RESULT 1
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

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Query Match 100.0%; Score 204; DB 9; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 2.1e-62;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60  
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Db 520 GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579





Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60  
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QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGATTTGGTACCAAGTCAGTCTTTTGT 120  
Db 673 GAGTTAGCTAGTGTGGCTCTACTACACAGGGCTGATGATCAAGTGAATGCTTTTGT 732

QY 121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTGATCGTCCCTGGTGCACAAACACAGCGA 180  
Db 733 TGTGGGGGAAACTGAAAAATTGGGAACCTGTGATCGTCCCTGGTGCACAAACACAGGAGA 792

QY 181 CACTTTCCTAAATGCTCTTTTGT 204  
Db 793 CACTTTCCTAAATGCTCTTTTGT 816

RESULT 5  
US-09-974-592-9  
; Sequence 9, Application US/09974592  
; Patent No. US2002012121A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: MacKenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009004  
; CURRENT APPLICATION NUMBER: US/09/974,592  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 09/617,053  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0.  
; SEQ ID NO 9  
; LENGTH: 2691  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-974-592-9

Query Match 84.3%; Score 172; DB 10; Length 2691;  
Best Local Similarity 90.2%; Pred. No. 5.2e-51;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60  
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Db 1218 GAGTTAGCTAGTGTGGCTCTACTACACAGGGCTGATGATCAAGTGAATGCTTTTGT 1277

QY 121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTGATCGTCCCTGGTGCACAAACACAGCGA 180  
Db 1278 TGTGGGGGAAACTGAAAAATTGGGAACCTGTGATCGTCCCTGGTGCACAAACACAGGAGA 1337

QY 181 CACTTTCCTAAATGCTCTTTTGT 204  
Db 1338 CACTTTCCTAAATGCTCTTTTGT 1361

RESULT 6  
US-09-201-936-5  
; Sequence 5, Application US/09201936  
; Publication No. US20020187946A1

; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: MacKenzie, Alexander E  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201,936  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2676  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (2470)...(2470)  
; OTHER INFORMATION: N may be any nucleotide  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (2476)...(2476)  
; OTHER INFORMATION: N may be any nucleotide  
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; OTHER INFORMATION: N may be any nucleotide  
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; LOCATION: (2602)...(2602)  
; OTHER INFORMATION: N may be any nucleotide  
US-09-201-936-5

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Best Local Similarity 67.0%; Pred. No. 6.4e-20;  
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60  
Db 693 GAAATGCCAGATTACTTACTTTTCAGACATGGCCA---TTGACTTTTCTGTCGCCAACA 749

QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGATTTGGTACCAAGTCAGTCTTTTGT 120  
Db 750 GATCGGCAGCAGCAGCGCTTTTACTACATAGACCTGGAGACAGAGTGGCTTGTCTTGGCC 809

QY 121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTGATCGTCCCTGGTGCAGAACACAGCGA 180  
Db 810 TGTGGTGGAAATTTGACCAATTTGGNACCGAGGATATGCTATGTCAGAACACCTCAGA 869

QY 181 CACTTTCCTAAATGCTCTTTTGT 203  
Db 870 CATTTCCTAAATGCTCTTTTGT 892

RESULT 7  
US-09-954-531-16  
; Sequence 16, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531

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; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-16

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Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

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QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGTATTTGGTACCAAGTGCAGTGTCTTTGT 120
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Db 1286 GATCTGGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACAGATGGCTTGTCTTTGCC 1345

QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGTATCGTGCCTGGTGCAGAACACAGCGGA 180
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QY 181 CACTTTCCTAATGCTTTTGT 203
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RESULT 8
US-09-954-456-1635
; Sequence 1635, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cano
; FILE REFERENCE: 589290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-16
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

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Best Local Similarity 67.0%  Pred. No. 6.8e-20;
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

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Db 1229 GAAATGCCAGATTACTTACTTTTCAGACATGGCCA---TTGACTTTTCTGTGCGCAACA 1285

QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGTATTTGGTACCAAGTGCAGTGTCTTTGT 120
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Db 1286 GATCTGGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACAGATGGCTTGTCTTTGCC 1345

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Db 1346 TGTGTGGAAGAACTGAGCAATTTGGAACTGAGGATAATGCTATGTCAGAACACCTGAGA 1405

QY 181 CACTTTCCTAATGCTTTTGT 203
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Db 1406 CATTTCCTCAATGCCATTAT 1428

RESULT 9
US-09-974-592-5
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

Query Match          41.5%  Score 84.6; DB 10; Length 6669;
Best Local Similarity 67.0%  Pred. No. 9.4e-20;
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
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Db 4725 GAAATGCCAGATTACTTACTTTTCAGACATGGCCA---TTGACTTTTCTGTGCGCAACA 4781

QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGTATTTGGTACCAAGTGCAGTGTCTTTGT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4782 GATCTGGCAGCAGGAGGCTTTTACTACATAGGACCTGGAGACAGATGGCTTGTCTTTGCC 4841

QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGTATCGTGCCTGGTGCAGAACACAGCGGA 180
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Db 4842 TGTGGTGAATAATGAGCAATGGACCAAGGATATGCTATGTCTAGACACCTGAGA 4901

Qy 181 CACTTCTCAATGCTCTTTGT 203  
Db 4902 CATTTTCCCAATGCCCATTTAT 4924

RESULT 10  
US-09-756-692-3493/c  
; Sequence 3493, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796.692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3493  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-756-692-3493

Query Match 38.4%; Score 78.4; DB 9; Length 240;  
Best Local Similarity 68.1%; Pred. No. 3.7e-18;  
Matches 109; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 44 CTCACCTAACCCCAAGAGAGTAGCAAGTGTGGAGCTCTACTACACAGGTATTTGGTACC 103  
Db 233 CTTTTCCTGCGCAACAGATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACA 174  
Qy 104 AAGTGCAGTCTTTTGTGTGGTGAACCTGAAATTTGGAACCTTTGTATCTGCTGCT 163  
Db 173 GAGTGGCTTGTGTCCTGCTGGTGAATTTGAGCAATTTGGCAATTTGGCAATTAATGCTA 114  
Qy 164 GGTCAACACAGGCGACACTTTCTTAATGCTTTTGT 203  
Db 113 TGTCAACACCTGAGACATTTTCCCAATGCCCATTTAT 74

RESULT 11  
US-09-756-692-6687  
; Sequence 6687, Application US/09796692

; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE  
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796.692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6687  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-756-692-6687

Query Match 37.6%; Score 76.8; DB 9; Length 240;  
Best Local Similarity 67.5%; Pred. No. 1.4e-17;  
Matches 108; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 44 CTCACCTAACCCCAAGAGAGTAGCAAGTGTGGAGCTCTACTACACAGGTATTTGGTACC 103  
Db 8 CTTTTCCTGCGCAACAGATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACA 67  
Qy 104 AAGTGCAGTCTTTTGTGTGGTGAACCTGAAATTTGGAACCTTTGTATCTGCTGCT 163  
Db 68 GAGTGGCTTGTGTCCTGCTGGTGAATTTGGCAATTTGGCAATTAATGCTA 127  
Qy 164 GGTCAACACAGGCGACACTTTCTTAATGCTTTTGT 203  
Db 128 TGTCAACACCTGAGACATTTTCCCAATGCCCATTTAT 167

RESULT 12  
US-09-974-592-13  
; Sequence 13, Application US/09974592  
; Patent No. US20020120121A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: MacKenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE

```

; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-13

```

Query Match	36.5%	Score 74.4;	DB 10;	Length 3151;
Best Local Similarity	62.2%	Pred. NO. 2.9e-16;		
Matches 117; Conservative	0;	Mismatches 71;	Indels 0;	Gaps 0;
QY	7	GCTAGATTAAAGTCCTTTGACAACTGGCCGACGATATGCTACCTAACCCCAAGAGAGTTA	66	
Db	1568	GCTCGATTGAGGACATTTCTGTACTGGCCACCTAGTGTCTCTGTTTCAGCCCGACGACGTT	1627	
QY	67	GCAAGTGCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGTGGT	126	
Db	1628	GCAAGTGCTGGATTCTATTACGTGGATGCGAATGATGATGTCAAGTGCCTTTTGTGTGAT	1687	
QY	127	GGAACACTGAAATTCGGGAACCTTGTCGTGCTCGCTGGTCAGACACACAGCGCACATTT	186	
Db	1688	GGTGGCTTTGAGTGTGGGAACCTTGGAGTAGACCCCTGGATAGAACACGCCAAATGGTTT	1747	
QY	187	CCTAATTG	194	
Db	1748	CCAAGGTG	1755	

```

RESULT 13
US-09-201-936-41
; Sequence 41, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; AND DETECTION METHODS
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-41

```

Qy	67	GCAAGTCTGGACCTCTACTACACAGTATTGGTGACCAAGTGCAGT	TCCTTTTGTGTGGT	126
Db	929	GCAAGTCTGGATTTCTATTACGTGGATCGCAATGATGATCAAGT	GCCTTTGTGTGAT	988
Qy	127	GGAAGACTGAARAATTGGGAACCTTGTGATCGTCTGGTCAGAACACAGCGCAGCTTT	186	
Db	989	GGTGGCTTGAGATGTTTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCAAATGGTTT	1048	
Qy	187	CCTAATTG	194	
Db	1049	CCAAAGGTG	1056	

```

RESULT 14
US-09-778-927A-21
  : Sequence 21, Application US/09778927A
  : Patent No. US20020068342A1
  : GENERAL INFORMATION:
  : APPLICANT: KHOSRAVI, Ramel et.al.
  : TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID
  : TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
  : FILE REFERENCE: 2786-0150P
  : CURRENT APPLICATION NUMBER: US/09/778,927A
  : CURRENT FILING DATE: 2001-02-08
  : PRIOR APPLICATION NUMBER: IL 134453
  : PRIOR FILING DATE: 2000-02-09
  : PRIOR APPLICATION NUMBER: IL135341
  : PRIOR FILING DATE: 2000-03-29
  : NUMBER OF SEQ ID NOS: 81
  : SOFTWARE: PatentIn Ver. 2.1
  : SEQ ID NO 21
  : LENGTH: 2291
  : TYPE: DNA
  : ORGANISM: Homo sapiens
  : FEATURE:
  : NAME/KEY: misc_feature
  : LOCATION: (1)..(2291)
  : OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-21

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RESULT 15  
US-09-201-936-7  
: Sequence 7, Application US/09201936  
: Publication No. US20020187946A1  
: GENERAL INFORMATION:  
: APPLICANT: Korneluk, Robert G.  
: APPLICANT: Mackenzie, Alexander E.  
: APPLICANT: Baird, Stephen  
: APPLICANT: Liston, Peter  
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
: TITLE OF INVENTION: PROBES, AND DETECTION METHODS

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; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match      34.4%  Score 70.2; DB 9; Length 2580;
Best Local Similarity 62.6%  Pred. No. 8.4e-15;
Matches 127; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY      1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      787 GAAGAAGCCAGATTCTTACCTACCATATGTGGCCA---TTAACTTTTGTGCACCATCA 843

QY      61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTGT 120
        || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      844 GAATTGGCAGAGCTGGTGTATATATAGGACCTGGAGATAGGGTAGCCCTGCTTTGCC 903

QY      121 TGTGTGGAAGAACTGAAAATTTGGAACTTGTGATCGTGTGCTGAGACACAGGCGGA 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      904 TGTGTGGGAGCTCAGTAACTGGGACCAAGGATGATGCTATGTCAGACACCGGAGG 963

QY      181 CACTTTCCTAATGCTTCTTTGT 203
        || ||||| ||||| |||||
Db      964 CATTTCCCAACTGTCCATTTT 986
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Search completed: April 16, 2003, 01:02:27  
Job time : 54.0521 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds  
(without alignments)  
3384.833 Million cell updates/sec

Title: US-09-654-743-46  
Perfect score: 204  
Sequence: 1 gaagaagctagattaaagtc.....ttcctaattgcttttgggt 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	822	12	BG502660
2	180.6	88.5	1041	13	BM459898
3	171	83.8	436	9	AI326613
4	163	79.9	375	9	AA097958
5	149	73.0	1020	13	BM554544
6	123.8	60.7	1130	13	BM553272

7	104.4	51.2	742	13	BI829221
8	84.6	41.5	557	9	AI051610
9	84.6	41.5	886	14	BQ652590
10	79.8	39.1	768	13	BM423292
11	79.2	38.8	593	13	BJ096099
12	78.2	38.3	567	13	BI961039
13	76.6	37.5	512	13	BI326908
14	75.6	37.1	459	13	BM446366
15	74.2	36.4	959	13	BM458775
16	72	35.3	298	12	BF016190
17	71.2	34.9	673	9	AL640849
18	70.2	34.4	401	12	BF095673
19	70.2	34.4	422	10	AW898626
20	70.2	34.4	889	14	BO720079
21	70.2	34.4	895	14	BQ884287
22	69.6	34.1	286	9	AA473594
23	68.8	33.7	450	12	BG729302
24	68.8	33.7	595	9	AI558531
25	68.6	33.6	649	10	AW949508
26	68.2	33.4	590	10	BE268377
27	68.2	33.4	837	12	BG743309
28	66.4	32.5	681	12	BF611032
29	66.2	32.5	851	13	BI253303
30	66.2	32.5	896	14	BO439248
31	65.4	32.1	611	13	BM536852
32	63.2	31.0	592	13	BJ059822
33	63.2	31.0	936	14	C81977
34	60.2	29.5	441	13	BM312708
35	60.2	29.5	563	9	AA702174
36	60.2	29.5	652	10	AV704923
37	60	29.4	953	17	CNS04211
38	59.4	29.1	395	9	AI552965
39	58.2	28.5	354	9	AA354707
40	57	27.9	302	14	B83677
41	57	27.9	341	10	AW375598
42	57	27.9	354	10	AW375594
43	57	27.9	402	10	AW846507
44	57	27.9	531	10	AW375599
45	57	27.9	532	10	AW846425

## ALIGNMENTS

RESULT 1  
BG502660

LOCUS 602549490F1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4657102 5', linear EST 27-MAR-2001  
DEFINITION BG502660 mRNA sequence.

ACCESSION BG502660  
VERSION BG502660.1 GI:13464177  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 822)  
AUTHORS NIH-MGC: <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Prepared by: The I.M.A.G.E. Consortium, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1449 row: c column: 23  
High quality sequence stop: 670.

FEATURES  
source 1..822  
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4657102"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT 236 a 161 c 201 g 222 t 2 others
ORIGIN

Query Match 100.0%; Score 204; DB 12; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.1e-59;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGA 60
DB 337 GAAGAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGA 396
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120
DB 397 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 456
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACCAACACAGCGCA 180
DB 457 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACCAACACAGCGCA 516
QY 181 CACTTCTCTAATTCCTCTTTGT 204
DB 517 CACTTCTCTAATTCCTCTTTGT 540

RESULT 2
BM459898
LOCUS BM459898
DEFINITION ACENOCOURT_6422054 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
5', mRNA sequence.
ACCESSION BM459898
VERSION BM459898
KEYWORDS EST.
SOURCE BM459898.1 GI:18508938
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1041)
NTH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L1AM12215 row: d column: 08
High quality sequence stop: 567.
Location/Qualifiers
1. .1041
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:5532247"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."
BASE COUNT 297 a 208 c 266 g 269 t 1 others
ORIGIN

Query Match 88.5%; Score 180.6; DB 13; Length 1041;
Best Local Similarity 92.6%; Pred. No. 3e-51;
Matches 189; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GAGAGAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGA 60
DB 553 GAGAGAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGA 612
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120
DB 613 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 672
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACCAACACAGCGCA 180
DB 673 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACCAACACAGCGCA 732
QY 181 CACTTCTCTAATTCCTCTTTGT 204
DB 733 CACTTCTCTAATTCCTCTTTGT 756

RESULT 3
AI326613
LOCUS AI326613
DEFINITION IMAGE:550702 5' similar to SW:TAPEX_MOUSE Q60989 X-LINKED INHIBITOR OF APOPTOSIS PROTEIN ;, mRNA sequence.
ACCESSION AI326613
VERSION AI326613
KEYWORDS EST.
SOURCE AI326613.1 GI:4061042
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 436)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:331494
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 417.
Location/Qualifiers
1. .436
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/clone_lib="Stratagene mouse Tcell 937311"

```

## FEATURES

source

```

/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG
3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGT 3'"
BASE COUNT      119 a   92 c   108 g   116 t   1 others
ORIGIN

Query Match      83.8%; Score 171; DB 9; Length 436;
Best Local Similarity 89.7%; Pred. No. 4.1e-48;
Matches 183; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGCTATGCTCATTTAACCCCAAGA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGTATTGTGACCAAGTCAGTGCCTTTTGT 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGTTAGCTAGTCGTGGCTCTACTACACAGGGCTGATGATCAAGTGCATGCTTTTGT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGTGGAAGAACTGAAAAATGGGAACCTTGTGATCGTGCCTGTCAGACACACAGGGCA 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGTGGGGAAACTGAAAAATGGGAACCTGTGATCGTGCCTGTCAGACACACAGGAGA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CACTTTCCTAATGCTTTTGT 204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CACTTTCCTAATGCTTTTGT 384
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 4
AA097958
LOCUS      AA097958      375 bp      mRNA      linear      EST 15-FEB-1997
DEFINITION      m83e12.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 5' similar to TR:G1145261 G1145261 MIHA. ;, mRNA
sequence.
ACCESSION      AA097958
VERSION        AA097958.1 GI:1643511
KEYWORDS       EST.
SOURCE         house mouse.
ORGANISM       Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE          1 (bases 1 to 375)
JOURNAL        Maier, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
COMMENT        Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
This clone is available royalty-free through LNL; contact the
WashU-HHMI Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:331494
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 191.
FEATURES       Location/Qualifiers
source         1..375
               /organism="Mus musculus"
               /db_xref="taxon:10090"
               /clone="IMAGE:550702"
               /clone_lib="Stratagene mouse Tcell 937311"
               /tissue_type="Tcell"

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/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG
3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGT 3'"
BASE COUNT      109 a   86 c   89 g   91 t
ORIGIN

Query Match      79.9%; Score 163; DB 9; Length 375;
Best Local Similarity 89.7%; Pred. No. 2.3e-45;
Matches 175; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGCTATGCTCATTTAACCCCAAGA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCAAGTCGTGGACTCTACTACACAGGTATTGTGACCAAGTCAGTGCCTTTTGT 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGTTAGCTAGTCGTGGCTCTACTACACAGGGCTGATGATCAAGTGCATGCTTTTGA 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGTGGAAGAACTGAAAAATGGGAACCTTGTGATCGTGCCTGTCAGACACACAGGGCA 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGTGGGGAAACTGAAAAATGGGAACCTGTGATCGTGCCTGTCAGACACACAGGAGA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CACTTTCCTAATGTC 195
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CACTTTCCTAATGTC 375
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
BM554544
LOCUS      BM554544      1020 bp      mRNA      linear      EST 20-FEB-2002
DEFINITION      AGENCOURT_6545864 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742590
5', mRNA sequence.
ACCESSION      BM554544
VERSION        BM554544.1 GI:18794228
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 1020)
JOURNAL        NIH-MGC http://mgi.mci.nih.gov/.
COMMENT        National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM12760 row: p column: 15
High quality sequence stop: 730.
FEATURES       Location/Qualifiers
source         1..1020
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:5742590"
               /clone_lib="NIH_MGC_119"
               /tissue_type="medulla"
               /lab_host="DH10B"
               /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber

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QY 1 GAAGAGCTAGATTA - AAGTCCTTTCAGAACT - GGCCAGACTATGC - TCACCTAACCCCA 57

||||| 503 GAAGAGCTAGATTACAACTGCTTTCACAACTGGCCAGCCCTCGCGCACTTGAACCCG 562

QY 58 AGAGAGTTAGCAAGTCTGGACTCTACTACACAGGTA-TTGGTGACCAAGTGCAGTGCTT 116

Db 563 AGAGAGCTGGCAGTCTGGCTGTACTACACAGGCACTTGTATGACCAAGTGCAGTGCTT 622

QY 117 TTGTGTGTGGTGAACAACTGAAATTTGGAACTTGTGTATCGTGGCTGTGACAAACACA- 175

Db 623 CTGTGTGGCGGAAACTGAAACTTGGGAACCTGTGTATCGTGGCTGTGACAAACAC 682

QY 176 TGGCAGACTTCTCTAATGCTCTT 201

Db 683 GGAGACATTTCTAATGGTCTT 708

RESULT 8  
LOCUS AI051610/c 557 bp mRNA linear EST 10-JUL-1998  
DEFINITION oz02c09.x1 Soares fetal\_liver\_spleen.INFLS.S1 Homo sapiens CDNA clone IMAGE:1674160 3' similar to SW:IAPI\_HUMAN Q13489 INHIBITOR OF APOPTOSIS PROTEIN 1 ; mRNA sequence.

ACCESSION AI051610  
VERSION AI051610  
KEYWORDS AI051610.1 GI:3307144  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 557)  
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40ml3 fwd. Et from Amersham  
High quality sequence stop: 436.

FEATURES  
Location/Qualifiers  
1..557  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Soares\_fetal\_liver\_spleen\_INFLS\_S1"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGAAGAAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 162 a 101 c 120 g 174 t  
ORIGIN  
Query Match 41.5%; Score 84.6; DB 9; Length 557;  
Best Local Similarity 67.0%; Pred. No. 4.1e-18;  
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 GAAGAGCTAGATTAAAGTCTCTTCAGAACTGGCCAGCACTATGCTCACTAACCCCAAGA 60

Db 396 GAAATGCCAGATTACTTACTTCTTCAGACATGGCCA---TTGACTTTCTGTGCGCAACA 340

QY 61 GAGTTAGCAAGTCTGGACTTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120

Db 339 GATCTGGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACAGAGTGGCTTGTGCTT 280

QY 121 TGTGTGGTGGTAAATTTGGAACTTGTGTATCGTGGCTGGTTCAGAAACACAGGCGA 180

Db 279 TGTGTGGTGGTAAATTTGGCAATTTGGAACTGGAGGATAATGCTATGTCAGAACACCTGAGA 220

QY 181 CACTTTCCTTAATTTGCTTCTTGT 203

Db 219 CATTTCCTCCCAATGCCCAATTAT 197

RESULT 9  
LOCUS BQ652590 886 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8287942 NIH\_MGC\_100 Homo sapiens 5' mRNA sequence.

ACCESSION BQ652590  
VERSION BQ652590.1 GI:21776762  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 886)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CGAP (Stanford)  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LCM2508 row: g column: 18  
High quality sequence stop: 638.

FEATURES  
Location/Qualifiers  
1..886  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NIH\_MGC\_100"  
/tissue\_type="hepatocellular carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: pOB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 255 a 193 c 186 g 250 t 2 others  
ORIGIN  
Query Match 41.5%; Score 84.6; DB 14; Length 886;  
Best Local Similarity 67.0%; Pred. No. 5.2e-18;  
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 GAAGAGCTAGATTAAAGTCTCTTCAGAACTGGCCAGCACTATGCTCACTAACCCCAAGA 60

Db 239 GAAATGCCAGATTACTTACTTCTTCAGACATGGCCA---TTGACTTTCTGTGCGCAACA 295

QY 61 GAGTTAGCAAGTCTGGACTTACTACACAGTATTGGTGACCAAGTGCAGTGCTTTTGT 120

Db 296 GATCTGGCAAAAGCAGGCTTTTACTACATAGGACTGGAGACAGAGTGGCTTGTGCTT 355

QY 121 TGTGTGGTGAACCTGAAAATTTGGAACTTGTGTATCGTGGCTGTGACAAACAGGCGA 180

Db 356 TGTGTGGTGAATTTGAGCAATTTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGA 415

```

QY 181 CACTTCCCTAATGCTCTTTGT 203
Db 416 CATTTCCTCAATGCCCATTTAT 438

RESULT 10
LOCUS BM423292 768 bp mRNA linear EST 29-JAN-2002
DEFINITION PLATE4_F12 Rhesus Macaca mulatta cDNA, mRNA sequence.
ACCESSION BM423292
VERSION BM423292.1 GI:18392786
KEYWORDS EST.
SOURCE rhesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 768)
AUTHORS Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
Expressed sequence tags from Rhesus macaque spleen
Unpublished (2002)
Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
PLATE4_F12 768 bases; 37.1 mean phred score.
FEATURES
Location/Qualifiers
1..768
/organism="Macaca mulatta"
/db_xref="taxon:9544"
/clone_lib="Rhesus"
/tissue_type="spleen"
/dev_stage="adult"
/note="Vector: pBluescript SK; SV40-associated
centroblastic non-Hodgkin's lymphoma"
BASE COUNT 216 a 161 c 174 g 217 t
ORIGIN
Query Match 39.1%; Score 79.8; DB 13; Length 768;
Best Local Similarity 65.5%; Pred. No. 2.2e-16;
Matches 133; Conservative 0; Mismatches 67; Indels 3; Gaps 1:
QY 1 GAAGAAGCTAGATTAAAGTCCTTTGAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGA 60
Db 307 GAAAAGCCAGATTACTTACTTTTCAGACGTGGCCA---TTGACTTTTCTGTGCGCAACA 363
QY 61 GAGTTAGCAAGTCTGGACTCTACTACAGAGTATGGTGCACCAAGTGCAGTGCCTTTTGT 120
Db 364 GATCTGGCAAGACGAGCTTTTACGTGGACCTGGAGACAGAGTGGCTTGTGCTTGGC 423
QY 121 TGTGGTGGAAACTGAAATTTGGGACCTTGTGATCGTGGCTGGTGCACCAACAGCGCA 180
Db 424 TGTGGCGGAAATTTGACAACTGGGACCAAGGATTAATGCAATGTGCAAGACCTGAGA 483
QY 181 CACTTTCCTAATGCTCTTTGT 203
Db 484 CATTTCCTCAATGCCCATTTAT 506

RESULT 11
LOCUS BJ096099 593 bp mRNA linear EST 12-DEC-2001
DEFINITION BJ096099 NIBB Mochii normalized xenopus early gastrula library
ACCESSION BJ096099
VERSION BJ096099.1 GI:17596868
KEYWORDS EST.
SOURCE African clawed frog.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 593)
AUTHORS Vandenplas, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E.,
Gingle, A.R., Pratt, L.H. and Moore, J.N.
An EST database from equine (Equus caballus) monocytes
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210

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ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 593)
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..593
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL152K19"
/clone_lib="NIBB Mochii normalized
library"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett
and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 175 a 129 c 137 g 152 t
ORIGIN
Query Match 38.8%; Score 79.2; DB 13; Length 593;
Best Local Similarity 72.9%; Pred. No. 3.1e-16;
Matches 102; Conservative 0; Mismatches 38; Indels 0; Gaps 0:
QY 1 GAAGAAGCTAGATTAAAGTCCTTTGAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGA 60
Db 453 GAGGAGGCCAGACTGCAAAACATTTCAAACTGGCCAGGTATTCCTCCGTTAATGCCAAA 512
QY 61 GAGTTAGCAAGTCTGGACTCTACTACAGAGTATGGTGCACCAAGTGCAGTGCCTTTGT 120
Db 513 GAGCTTGCAATGCAGGTCTCTTTATACAGCATCAGCACCACCAAGTCAATGCTTTGT 572
QY 121 TGTGTGGAAACTGAAAAA 140
Db 573 TGTGTGGAAACTAATGAA 592

RESULT 12
LOCUS BI961039 567 bp mRNA linear EST 22-OCT-2001
DEFINITION MONOL_5_C10.B1_A005 Monocytes (MONOL) Equus caballus cDNA, mRNA
sequence.
ACCESSION BI961039
VERSION BI961039.1 GI:16319242
KEYWORDS EST.
SOURCE horse.
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 567)
AUTHORS Vandenplas, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E.,
Gingle, A.R., Pratt, L.H. and Moore, J.N.
An EST database from equine (Equus caballus) monocytes
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210

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Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyMix or T7 sequencing primer, are presented as the reverse complement.  
Seq primer: JEN REV  
High quality sequence stop: 534  
POLYA-No.

FEATURES  
source  
1. .567  
Location/Qualifiers  
/organism="Equus caballus"  
/db\_xref="taxon:9796"  
/clone\_lib="Monocytes (MONO1)"  
/cell\_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"  
/note="Vector: pBluescript SK(-) from Lambda ZapII; Site.1: XhoI; Site.2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZapII. Clones to be sequenced were prepared by mass excision."  
BASE COUNT 147 a 130 c 136 g 154 t  
ORIGIN

Query Match 38.3%; Score 78.2; DB 13; Length 567;  
Best Local Similarity 65.0%; Pred. No. 6.8e-16;  
Matches 132; Conservative 0; Mismatches 68; Indels 3; Gaps 1;  
QY 1 GAAGAGCTAGATTAAAGCTCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60  
DB 96 GAAAAGCCAGATATCTACTTCCAGATGTGGCC---GCTGACCTTTCTGTGCCACACA 152  
QY 61 GAGTTAGCAAGTCTGGAGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGT 120  
DB 153 GATCTGCAAAAGCTGGCTTTTACTACATAGACCCGGGACAGAGTGGCTGCTTTGCC 212  
QY 121 TGTGTGGAAACATGAAAATTTGGGAACCTTGTGTGTCGTCCTGGTCAGAACACAGCGGA 180  
DB 213 TGTGTGGAAATTTGACAAATTTGGGAACCGAAGGATGATGCTATGTCGGAACACCTGGA 272  
QY 181 CACTTTCCTAATTCCTCTTTGT 203  
DB 273 CATTTCCCAACTGCGCGTTGT 295

RESULT 13  
LOCUS BI326908 512 bp mRNA linear EST 01-SEP-2001  
DEFINITION AR071E101SPBE10S Infected Porcine Spleen cDNA library Sus scrofa cDNA, mRNA sequence.  
ACCESSION BI326908  
VERSION BI326908.1 GI:15416611  
KEYWORDS EST.  
SOURCE pig.  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 512)  
AUTHORS Rink A., Santschi E.M. and Beattie C.W.  
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of Orthopedic Implant Associated Staphylococcus aureus Infection  
JOURNAL Unpublished (2001)  
COMMENT Contact: Rink A  
Department of Animal Biotechnology  
College of Agriculture, Biotechnology and Natural Resources,  
University of Nevada, Reno  
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA  
Tel: 775 784 1705  
Fax: 775 784 1375  
Email: arink@cabnr.unr.edu

Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The

adapter sequence is 'AATTCGGCAGGAG'.  
Location/Qualifiers  
1. .512  
/organism="Sus scrofa"  
/strain="crossbreed"  
/db\_xref="taxon:9823"  
/clone\_lib="Infected porcine Spleen cDNA library"  
/tissue\_type="Spleen"  
/cell\_type="mixed"  
/dev\_stage="28 days post infection, 5 month old castrated male"  
/lab\_host="SOLR"  
/note="Vector: pBSK; Site.1: Eco RI; Site.2: XhoI; Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCAGGAG'."

BASE COUNT 136 a 108 c 113 g 145 t 10 others  
ORIGIN

Query Match 37.5%; Score 76.6; DB 13; Length 512;  
Best Local Similarity 64.5%; Pred. No. 2.3e-15;  
Matches 131; Conservative 0; Mismatches 69; Indels 3; Gaps 1;  
QY 1 GAAGAAGCTAGATTAAAGCTCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60  
DB 79 GAAAAGCAGATATCTACTTCCAGATGTGGCC---TTGACCTTTCTGTGCCACGA 135  
QY 61 GAGTTAGCAAGTCTGGAGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGT 120  
DB 136 GATCTGCAAAAGCAGCTTTTACTACATAGACCTGGACAGAGTGGCTTGTTCGCC 195  
QY 121 TGTGTGGAAACATGAAAATTTGGGAACCTTGTGTGTCGTCCTGGTCAGAACACAGCGGA 180  
DB 196 TGTGTGGAAATTTGACAAATTTGGGAACCAAGGATGATGCTATGACAGAACACTTACGA 255  
QY 181 CACTTTCCTAATTCCTCTTTGT 203  
DB 256 CATTTCCCAACTGCGCCATTTT 278

RESULT 14  
LOCUS BM446366 459 bp mRNA linear EST 05-FEB-2002  
DEFINITION IL16H6.ab1 Bos taurus ileum #1 library Bos taurus cDNA, mRNA sequence.  
ACCESSION BM446366  
VERSION BM446366.1 GI:18530522  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 459)  
AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S.  
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)  
COMMENT Contact: Dr. Stephen Moore  
Beef Genomics Laboratory  
Dept of AFNS, University of Alberta  
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
Tel: 780 492 0169  
Fax: 780 492 4265  
Email: smoores@afns.ualberta.ca  
Insert Length: 459 Std Error: 0.00  
POLYA-No.

FEATURES  
source  
1. .459  
Location/Qualifiers



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1001.52 Seconds  
(without alignments)  
5753.635 Million cell updates/sec

Title: US-09-654-743-47  
Perfect score: 198  
Sequence: 1 tatgaagcagcgtctttac.....atccagggtcgaatatctg 198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hcg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pi.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rdt.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	198	100.0	1659	6	E31042	E31042 Method for
2	198	100.0	1659	9	HSU32974	U32974 Human IAP-1
3	198	100.0	2086	9	BC032729	BC032729 Homo sapi
4	198	100.0	2404	6	AX429575	AX429575 Sequence
5	198	100.0	2540	6	AR103281	AR103281 Sequence
6	198	100.0	2540	6	AX412118	AX412118 Sequence
7	198	100.0	2540	9	HSU45880	U45880 Human X-lin
8	198	100.0	3000	6	AX412131	AX412131 Sequence
9	198	100.0	5232	6	AR106397	AR106397 Sequence
10	198	100.0	5232	6	AR116599	AR116599 Sequence
11	180.4	91.1	1752	6	AX104956	AX104956 Sequence
12	180.4	91.1	1752	9	AF164681	AF164681 Homo sapi
13	180.4	91.1	154214	9	AC079753	AC079753 Homo sapi
14	179.4	90.6	1491	10	AF183429	AF183429 Rattus no
15	179.4	90.6	2468	10	AB033366	AB033366 Rattus no
16	179.4	90.6	3032	10	AF304334	AF304334 Rattus no
17	177.8	89.8	2032	10	AF304333	AF304333 Rattus no
18	174.6	88.2	1988	10	MMU36842	U36842 Mus musculu
19	173	87.4	2100	6	AX412124	AX412124 Sequence
20	169.8	85.8	2691	6	AR106400	AR106400 Sequence
21	169.8	85.8	2691	6	AR116702	AR116702 Sequence
22	169.8	85.8	2691	10	MMU88990	U88990 Mus musculu
23	166	83.8	711	6	AX104970	AX104970 Sequence
24	166	83.8	711	9	AY030052	AY030052 Pan trogl
25	166	83.8	1758	6	AX370787	AX370787 Sequence
26	166	83.8	1758	6	AX370789	AX370789 Sequence
27	166	83.8	4993	6	AX104968	AX104968 Sequence
28	166	83.8	4993	9	AF164682	AF164682 Homo sapi
29	166	83.8	144301	9	AC010467	AC010467 Homo sapi
30	166	83.8	165662	9	AC092070	AC092070 Homo sapi
31	164.4	83.0	711	6	AR121220	AR121220 Sequence
32	164.4	83.0	711	6	AR123871	AR123871 Sequence
33	164.4	83.0	2032	9	AF420440	AF420440 Homo sapi
34	162.8	82.2	711	6	AX104972	AX104972 Sequence
35	162.8	82.2	711	9	AY030053	AY030053 Gorilla g
36	146.6	74.0	187568	9	AP002967	AP002967 Homo sapi
37	145	73.2	184439	2	AP003085	AP003085 Homo sapi
38	132.6	67.0	327	4	AF458770	AF458770 Bos tauru
39	105	53.0	133391	9	HSJ31561	HSJ31561 Human DNA
40	105	53.0	201197	2	HS424712	HS424712 Homo sapien
41	100.4	50.7	1740	5	AF451854	AF451854 Gallus ga
42	96.8	48.9	158093	9	AL390123	AL390123 Human DNA
43	79.2	40.0	1770	10	AF183431	AF183431 Rattus no
44	78.6	39.7	2563	9	HUMSCP8	L49432 Homo sapien
45	78.6	39.7	2601	6	AR129833	AR129833 Sequence

ALIGNMENTS

RESULT 1  
E31042  
LOCUS E31042  
DEFINITION Method for screening substance inhibiting binding to XIAP.  
ACCESSION E31042  
VERSION E31042.1 GI:13017307  
KEYWORDS JP 1999326328-A/2.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1659)  
AUTHORS Kunihiro,M.  
TITLE Method for screening substance inhibiting binding to XIAP  
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;  
KUNIHIRO MATSUMOTO

E31042 1659 bp DNA linear PAT 18-JUN-2001  
Method for screening substance inhibiting binding to XIAP.



Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc.mc@hri.nih.gov  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Masfallo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 69 Row: 1 Column: 18  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4502142.

## FEATURES

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 /db\_xref="taxon:9606"  
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 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
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 YSEEARLKQFNPDPYAHLPTELASAGLYITGIDQVQFCGCGKLKNWPCDRAWS  
 EHRHFPNCFEVLGRNLNLRSESDAVSSDRNPNLPRNPMDYARIFFTGTWI  
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 GQYINNIHLTSLERCLVYRTEKTSLSRPRDDITFQNPWQEARMGFSFKDIKI  
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## CDS

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 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 QY 61 GCAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
 Db 931 GCAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 990  
 QY 121 GGAGGGCTAACTGATTTGGAGCCGAGTGAAGACCCCTTTGGGAACAACATGCTTAATGGTAT 180  
 Db 991 GGAGGGCTAACTGATTTGGAGCCGAGTGAAGACCCCTTTGGGAACAACATGCTTAATGGTAT 1050  
 QY 181 CCAGGGTGCAAAATATCTG 198  
 Db 1051 CCAGGGTGCAAAATATCTG 1068

## RESULT 4

## AX429575

## LOCUS

AX429575 2404 bp DNA linear PAT 21-JUN-2002

DEFINITION Sequence 38 from Patent WO0226820.  
 ACCESSION AX429575  
 VERSION AX429575.1 GI:21540833  
 KEYWORDS human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,  
 Reinhardt, M.W. and Zisman, S.  
 TITLE Transgenic drosophila melanogaster expressing beta amyloid  
 JOURNAL Patent: WO 0226820-A 38 04-APR-2002;  
 NOVARTIS ERFIND VERWALT GMBH (AT)  
 FEATURES Location/Qualifiers  
 source  
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 /db\_xref="taxon:9606"  
 BASE COUNT 759 a 372 c 525 g 748 t  
 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TATGAACGCGGATCTTTACTTTTGGGACATGGATATACAGTAAAGGAGCAGCTT 60  
 Db 827 TATGAACGCGGATCTTTACTTTTGGGACATGGATATACAGTAAAGGAGCAGCTT 886  
 QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
 Db 887 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 946  
 QY 121 GGAGGGCTAACTGATTTGGAGCCGAGTGAAGACCCCTTTGGGAACAACATGCTTAATGGTAT 180  
 Db 947 GGAGGGCTAACTGATTTGGAGCCGAGTGAAGACCCCTTTGGGAACAACATGCTTAATGGTAT 1006  
 QY 181 CCAGGGTGCAAAATATCTG 198  
 Db 1007 CCAGGGTGCAAAATATCTG 1024  
 RESULT 5  
 AR103281  
 LOCUS AR103281 2540 bp DNA linear PAT 14-FEB-2001  
 DEFINITION Sequence 1 from patent US 6087173.  
 ACCESSION AR103281  
 VERSION AR103281.1 GI:12814869  
 KEYWORDS Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2540)  
 AUTHORS Bennett, C. Frank, Ackermann, E. J. and Cowser, L. M.  
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression  
 JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
 FEATURES Location/Qualifiers  
 source  
 1. .2540  
 /organism="unknown"  
 BASE COUNT 781 a 415 c 571 g 773 t  
 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 0;  
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 Db 826 TATGAACGCGGATCTTTACTTTTGGGACATGGATATACAGTAAAGGAGCAGCTT 885  
 QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
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RESULT 6  
 AX412118 2540 bp DNA linear PAT 14-JUN-2002  
 LOCUS Sequence 218 from Patent WO0226968.  
 DEFINITION AX412118  
 ACCESSION AX412118  
 VERSION AX412118.1 GI:21444581  
 KEYWORDS

SOURCE human..  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
 TITLE Antisense iap nucleic acids and uses thereof  
 JOURNAL Patent: WO 0226968-A 218 04-APR-2002;  
 University of Ottawa (CA); Aegera Therapeutics Inc. (CA)

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 /note="XIAP"  
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 /db\_xref="GI:1184320"  
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BASE COUNT 781 a 415 c 570 g 773 t 1 others  
 ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120  
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QY 181 CCAGGGTGCAAAATATCTG 198  
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 Db 1006 CCAGGGTGCAAAATATCTG 1023  
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RESULT 7  
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 LOCUS Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete  
 DEFINITION cds.  
 ACCESSION U45880  
 VERSION U45880.1 GI:1184319  
 KEYWORDS

SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2540)  
 AUTHORS Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,  
 Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., MacKenzie, A.  
 and Korneluk, R.G.  
 TITLE Suppression of apoptosis in mammalian cells by XIAP and a related  
 family of IAP genes  
 JOURNAL Nature 379 (5563), 349-353 (1996)

MEDLINE 96149249  
 PUBMED 8552191  
 REFERENCE 2 (bases 1 to 2540)  
 AUTHORS Baird, S.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of  
 Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1,  
 Canada

FEATURES  
 source

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 YCEARLKSQFNQPOVAHLTPRELASAGLYYTGIDQVOCFCGCGKLKNWPCDRAMS  
 EHRHFPNCFVVLGRNLNIRSESDAYSSDRNPNSTNLRPNMADYEAEIFTEGTWI  
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CDS

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 misc\_feature 520..723  
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 misc\_feature 826..1020  
 /note="encodes BIR3"  
 misc\_feature 1381..1485  
 /note="encodes Ring Zinc Finger"

BASE COUNT 781 a 415 c 571 g 773 t  
 ORIGIN

Query Match 100.0%; Score 198; DB 9; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACATCTACGTTACAAAGGAGCAGCTT 60  
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Db 826 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACATCTACGTTACAAAGGAGCAGCTT 885  
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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120  
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Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 945  
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QY 181 CCAGGGTGCAAAATATCTG 198  
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RESULT 8  
 AX412131 3000 bp DNA linear PAT 14-JUN-2002  
 LOCUS Sequence 231 from Patent WO0226968.  
 DEFINITION AX412131  
 ACCESSION AX412131  
 VERSION AX412131.1 GI:21444588  
 KEYWORDS human..  
 SOURCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
TITLE Antisense iap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 231 04-APR-2002;  
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)

FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:9606"  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2e-44;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60  
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Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 120  
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Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180  
Db 1602 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 1661

Qy 181 CCAGGTCGAATATCTG 198  
Db 1662 CCAGGTCGAATATCTG 1679

RESULT 9  
AR106397  
LOCUS AR106397 5232 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 3 from patent US 6107041.  
ACCESSION AR106397  
VERSION AR106397.1 GI:12820927  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL Patent: US 6107041-A 3 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..5232  
/organism="unknown"  
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.1e-44;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 120  
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 945

Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180  
Db 945 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 1005

Qy 181 CCAGGTCGAATATCTG 198  
Db 1006 CCAGGTCGAATATCTG 1023

RESULT 11  
AX104956  
LOCUS AX104956 1752 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 1 from Patent WO0123368.  
ACCESSION AX104956  
VERSION AX104956.1 GI:13921153  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1752)  
AUTHORS Duckett, C. and Mir, S.S.  
TITLE Members of the iap gene family  
JOURNAL Patent: WO 0123588-A 1 05-APR-2001;  
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES Location/Qualifiers  
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847..1197  
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/db\_xref="GI:13921154"

CDS

Qy 181 CCAGGTCGAATATCTG 198  
Db 1006 CCAGGTCGAATATCTG 1023

RESULT 10  
AR116699  
LOCUS AR116699 5232 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6133437.  
ACCESSION AR116699  
VERSION AR116699.1 GI:14097021  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..5232  
/organism="unknown"  
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others  
ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 2.1e-44;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTTACTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60  
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Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 120  
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTGCTTTCACTGTGGA 945

Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180  
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Qy 181 CCAGGTCGAATATCTG 198  
Db 1006 CCAGGTCGAATATCTG 1023

RESULT 11  
AX104956  
LOCUS AX104956 1752 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 1 from Patent WO0123368.  
ACCESSION AX104956  
VERSION AX104956.1 GI:13921153  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1752)  
AUTHORS Duckett, C. and Mir, S.S.  
TITLE Members of the iap gene family  
JOURNAL Patent: WO 0123588-A 1 05-APR-2001;  
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
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CDS

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ORIGIN

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Best Local Similarity 94.4%; Pred. No. 1.7e-39;  
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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DB 499 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATACCTAGTTAAACAAGGACGCTT 558  
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCTGATAAGTAAAGTGCCTTTCACTGTGGA 120  
DB 559 TCAAGAGCTGGATTTATGCTTTAGGTGAAGCTGATAAGTAAAGTGCCTTTCACTGTGGA 618  
QY 121 GGAGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180  
DB 619 GGGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACACATGATAAATGGCAT 678  
QY 181 CCAGGTGCAAAATATCTG 198  
DB 679 CCAGGTGTAATATCTG 696

RESULT 12  
AF164681 AF164681 1752 bp DNA linear PRI 31-JUL-2001  
LOCUS  
DEFINITION Homo sapiens IAP-like protein 3 (ILP3) gene, complete cds.  
ACCESSION AF164681  
VERSION AF164681.1 GI:15042061  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1752)  
AUTHORS Mir, S.S. and Duckett, C.S.  
TITLE Molecular cloning of human homologs of IAP-like protein  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1752)  
AUTHORS Mir, S.S. and Duckett, C.S.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUL-1999) Metabolism Branch, National Cancer  
Institute, 10 Center Drive, Room 6B-05, Bethesda, MD 20892-1578,  
USA

FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
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/note="similar to Homo sapiens ILP"  
/codon\_start=1  
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QEA"

BASE COUNT 530 a 299 c 385 g 538 t  
ORIGIN

Query Match 91.1%; Score 180.4; DB 9; Length 1752;

Best Local Similarity 94.4%; Pred. No. 1.7e-39;  
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATACCTAGTTAAACAAGGACGCTT 60  
DB 499 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATACCTAGTTAAACAAGGACGCTT 558  
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCTGATAAGTAAAGTGCCTTTCACTGTGGA 120  
DB 559 TCAAGAGCTGGATTTATGCTTTAGGTGAAGCTGATAAGTAAAGTGCCTTTCACTGTGGA 618  
QY 121 GGAGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180  
DB 619 GGGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACACATGATAAATGGCAT 678  
QY 181 CCAGGTGCAAAATATCTG 198  
DB 679 CCAGGTGTAATATCTG 696

RESULT 13  
AC079753 AC079753 154214 bp DNA linear PRI 01-MAR-2002  
LOCUS  
DEFINITION Homo sapiens BAC clone RP11-67L14 from 2, complete sequence.  
ACCESSION AC079753  
VERSION AC079753.7 GI:14318395  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 154214)  
AUTHORS Sulston, J.E. and Waterston, R.  
TITLE Toward a complete human genome sequence  
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
MEDLINE 99063792  
PUBMED 9847074

REFERENCE 2 (bases 1 to 154214)  
AUTHORS Andrews, S., Cotton, M., Doebber, A. and Rose, C.  
TITLE The sequence of Homo sapiens BAC clone RP11-67L14  
JOURNAL Unpublished (2001)  
REFERENCE 3 (bases 1 to 154214)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

REFERENCE 4 (bases 1 to 154214)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

REFERENCE 5 (bases 1 to 154214)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUL-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

REFERENCE 6 (bases 1 to 154214)  
AUTHORS Waterston, R.  
TITLE Direct Submission  
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
REFERENCE 7 (bases 1 to 154214)  
AUTHORS Waterston, R.

REFERENCE 8 (bases 1 to 154214)  
AUTHORS Waterston, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Jun 6, 2001 this sequence version replaced gi:14029079.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@genome.wustl.edu](mailto:sapiens@genome.wustl.edu)  
 ----- Summary Statistics -----  
 Center project name: H\_NH0067L14  
 -----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPII-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenoe, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
 VECTOR: pBAC3.6

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-725J3. Actual start of this clone is at base position 1 of RP11-67L14; actual end is at base position 154214 of RP11-67L14.

There are polymorphic base differences in the overlap between

RP11-67L14 and RP11-725J3.

#### FEATURES

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misc_feature	/chromosome="2"
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repeat_region	/clone_lib="RPII-11"
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misc_feature	1629..1748
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repeat_region	2589..3114
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repeat_region	/rpt_family="Alu"
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Db 1239 GGAGGGCTCAGGATTTGGAAAGCCAAAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1298  
QY 181 CCAGGGTGCAAAATATCT 197  
Db 1299 CCAGGGTGTAATATCT 1315

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 132.344 Seconds  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	1659	AAZ48862	Human XIAP coding
2	198	100.0	2404	AAK99405	DNA of APP related
3	198	100.0	2540	AAAT70836	Human apoptosis in
4	198	100.0	2540	AAA64901	Human X-linked inh
5	198	100.0	2540	ABK93869	Human CDNA encodin
6	198	100.0	3000	ABK93875	Human CDNA encodin
7	198	100.0	5232	AAV55038	Human XIAP coding
8	180.4	91.1	1752	AAAD03575	Human IAP-like pro
9	174.6	88.2	1988	AAAT72710	Mouse inhibitor of

10	173	87.4	2100	18	AAAT70839	Mouse apoptosis in
11	173	87.4	2100	24	ABK93872	Mouse cDNA encodin
12	169.8	85.8	2691	19	AAV55041	Murine XIAP coding
13	166	83.8	711	22	AAAD03582	Chimpanzee IAP-like
14	166	83.8	1758	24	ABK14677	Human inhibitor of
15	166	83.8	1758	24	ABK14678	Human inhibitor of
16	166	83.8	4993	22	AAAD03581	Human IAP-like pro
17	164.4	83.0	711	21	AAA06940	DNA encoding human
18	164.4	83.0	1559	24	ABK13197	Human testes speci
19	162.8	82.2	711	22	AAAD03583	Gorilla IAP-like p
20	157.8	79.7	578	20	AAAD02960	Human IL-1ra BAC c
21	131.4	66.4	802	20	AAAD03018	Human IL-1ra BAC c
22	96.8	48.9	302	24	ABQ58785	Human colon cancer
23	83	41.9	1402	20	AAAD03028	Human IL-1ra BAC c
24	78.6	39.7	2601	18	AAAT61591	Human c-IAP2, Hom
25	78.6	39.7	2666	18	AAAT70837	Human apoptosis in
26	78.6	39.7	2676	24	ABK93870	Human CDNA encodin
27	78.6	39.7	3076	18	AAAT72712	Human inhibitor of
28	78.6	39.7	3076	20	AAZ41005	Human cellular inh
29	78.6	39.7	3076	20	AAZ22096	Human cellular inh
30	78.6	39.7	3076	24	ABL62746	Breast cancer rela
31	78.6	39.7	3076	24	ABL66325	Lung cancer relate
32	78.6	39.7	3734	22	AAAC90972	Human API2-MIT chi
33	78.6	39.7	3734	24	ABK52387	DNA encoding cysti
34	78.6	39.7	6669	19	AAV55039	Human HIAP-1 codin
35	78.6	39.7	6669	24	ABK93876	Human CDNA encodin
36	74.4	37.6	1435	17	AAAT43709	Human inhibitor of
37	74.4	37.6	2580	18	AAAT70838	Human apoptosis in
38	74.4	37.6	2580	24	ABK93871	Human CDNA encodin
39	74.4	37.6	2589	18	AAAT61590	Human c-IAP1, Hom
40	74.4	37.6	3532	18	AAAT72711	Human inhibitor of
41	74.4	37.6	3532	20	AAZ22143	Human cellular inh
42	74.4	37.6	3532	24	ABN96857	Gene #3355 used to
43	74.4	37.6	3732	19	AAV55040	Human HIAP-2 codin
44	71.2	36.0	2862	18	AAAT61592	Murine c-IAP, Mus
45	71.2	36.0	3151	19	AAV55043	Murine HIAP-2 codi

## ALIGNMENTS

RESULT 1  
AAZ48862  
ID AAZ48862 standard; CDNA; 1659 BP.

AC AAZ48862;  
XX  
XX 24-MAR-2000 (first entry)  
DT Human XIAP coding sequence.

DE  
XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production;  
KW cell growth inhibitor; beta-amyloid protein deposition;  
KW immunosuppression; Transforming growth factor-beta; ds.

OS Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-0130378.

XX 13-MAY-1998; 98JP-0130378.

XX (MATS/) MATSUMOTO K.

XX WPI: 2000-078337/07.

XX P-PSDB; AAY59451.

PT Screening a substance which inhibits combination of the X-linked

PT inhibitor of apoptosis protein  
XX  
PS Disclosure; Page 28-30; 43pp; Japanese.  
XX  
XX This sequence encodes the human XIAP protein.  
CC The invention relates to a method for screening a substance inhibiting  
CC the formation of a complex between XIAP and TAB1, in which X-linked  
CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
CC activated kinase 1 (TAK1) binding protein (TAB1) and a substance to be  
CC tested are contacted with each other and then the presence or formation  
CC of a complex between XIAP and TAB1 is detected. The substance can be used  
CC as a drug for extracellular matrix protein production enhancement, cell  
CC growth inhibition, monocyte migration, physiologically active substance  
CC induction, immunosuppression, and beta-amyloid protein deposition. A  
CC substance inhibiting the formation of a complex between TAB1 and XIAP as  
CC well as between XIAP and TGF-beta (transforming growth factor-beta) type  
CC I and/or type II receptor is useful as a drug.  
XX  
SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
  
Query Match 100.0%; Score 198; DB 21; Length 1659;  
Best Local Similarity 100.0%; Pred. No. 1.7e-54;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TATGACGACCGATCTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 60  
DB 874 TATGACGACCGATCTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 933  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 120  
DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 993  
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAGACCCCTTGGGACACATGCTTAATGGTAT 180  
DB 994 GGAGGGCTAACTGATTTGAAGCCAGTGAGACCCCTTGGGACACATGCTTAATGGTAT 1053  
QY 181 CCAGGGTGCAAAATATCTG 198  
DB 1054 CCAGGGTGCAAAATATCTG 1071  
  
RESULT 2  
AAK99405  
ID AAK99405 standard; DNA; 2404 BP.  
XX  
XX  
AC AAK99405;  
XX  
XX 27-JUN-2002 (first entry)  
XX  
XX DNA of APP related human homologue hcp35211.  
XX  
XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;  
XX amyloid precursor protein; tissue-specific expression control; human APP;  
XX APP pathway modulator; gene therapy; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 692..1528  
XX /\*tag= a  
XX /product= "Protein of human homologue hcp35211"  
XX /note= "No start codon"  
XX  
XX WO200226820-A2.  
XX  
XX  
XX 04-APR-2002.  
XX  
XX 01-OCT-2001; 2001WO-EP11345.  
XX  
XX 29-SEP-2000; 2000US-236893P.  
XX 14-JUN-2001; 2001US-298309P.  
XX  
XX (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH;  
XX  
XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;  
XX Reinhardt MWM, Zusman S;  
XX  
XX WPI: 2002-315796/35.  
XX P-PSDB: AAO20511.  
XX  
XX New transgenic fly, containing DNA encoding an Abeta portion of human  
XX APP, useful for identifying agents which modulate the APP pathway and  
XX which can be used to treat Alzheimer's disease  
XX  
XX Example 4; Page 111; 129pp; English.  
XX  
XX The invention relates to a transgenic fly whose genome comprises DNA  
XX encoding a polypeptide having the Abeta portion of human amyloid  
XX precursor protein (APP), fused to a signal sequence. The DNA sequence  
XX encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in  
XX the specification. The DNA sequence is operably linked to a tissue-  
XX specific expression control sequence. Expression of the sequence gives  
XX the fly an altered phenotype. The purpose of the invention is for  
XX identifying agents that inhibit or promote the expression and/or function  
XX of genes or encoded polypeptides which modify the APP pathway. The agent  
XX is a compound, triple helix DNA, antisense oligonucleotide, double  
XX stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
XX to treat conditions such as Alzheimer's disease. The agent can be used as  
XX an APP pathway modulator or in gene therapy. This polynucleotide sequence  
XX represents the DNA of the APP related human homologue hcp35211.  
XX  
SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;  
  
Query Match 100.0%; Score 198; DB 24; Length 2404;  
Best Local Similarity 100.0%; Pred. No. 1.9e-54;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TATGACGACCGATCTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 60  
DB 827 TATGACGACCGATCTTACTTTTGGGACATGGATATCTACTCAGTTAAACAGGACGCTT 886  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 120  
DB 887 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTCACTGTGGA 946  
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAGACCCCTTGGGACACATGCTTAATGGTAT 180  
DB 947 GGAGGGCTAACTGATTTGAAGCCAGTGAGACCCCTTGGGACACATGCTTAATGGTAT 1006  
QY 181 CCAGGGTGCAAAATATCTG 198  
DB 1007 CCAGGGTGCAAAATATCTG 1024  
  
RESULT 3  
AAT70836  
ID AAT70836 standard; cDNA; 2540 BP.  
XX  
XX  
AC AAT70836;  
XX  
XX 02-SEP-1997 (first entry)  
XX  
XX Human apoptosis inhibitor xiap cDNA.  
XX  
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
XX XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
XX ischaemia; myocardial infarction; stroke;  
XX reperfusion injury; toxin-induced liver disease; gene therapy;  
XX diagnosis; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 34..1527  
XX /\*tag= a





KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytotatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX Homo sapiens.  
 OS  
 PN WO200226968-A2.  
 XX  
 XX 04-APR-2002.  
 PD  
 XX 27-SEP-2001; 2001WO-CA01379.  
 PF  
 XX 28-SEP-2000; 2000US-0672717.  
 PR  
 XX (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 PI  
 XX WPI: 2002-479562/51.  
 DR P-PSDB; ABG65663.  
 DR  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases -  
 PT  
 PS Disclosure; Fig 1; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 XX Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
 SQ  
 Query Match 100.0%; Score 198; DB 24; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTAGTAAAGTCTTCACTGTGGA 60  
 DB 826 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTAGTAAAGTCTTCACTGTGGA 885  
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATTAAGTCTTCACTGTGGA 120  
 DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATTAAGTCTTCACTGTGGA 945  
 QY 121 GGAGGGCTAACTGATTTGAGCCAGGAGCCCTTTGGGAAACCAATGCTTAATGCTAT 180  
 DB 946 GGAGGGCTAACTGATTTGAGCCAGGAGCCCTTTGGGAAACCAATGCTTAATGCTAT 1005  
 QY 181 CCAGGGTCCAAATATCTG 198  
 DB 1006 CCAGGGTCCAAATATCTG 1023

## RESULT 6

ABK93875  
 ID ABK93875 standard; cDNA; 3000 BP.  
 XX  
 AC ABK93875;  
 XX  
 XX 26-AUG-2002 (first entry)  
 DT  
 XX Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
 DE  
 XX  
 XX Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytotatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX Homo sapiens.  
 OS  
 XX WO200226968-A2.  
 PN  
 XX  
 XX 04-APR-2002.  
 PD  
 XX 27-SEP-2001; 2001WO-CA01379.  
 PF  
 XX 28-SEP-2000; 2000US-0672717.  
 PR  
 XX (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 PI  
 XX WPI: 2002-479562/51.  
 DR  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases -  
 PT  
 PS Example 2; Fig 15; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 XX Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 198; DB 24; Length 3000;  
 Best Local Similarity 100.0%; Pred. No. 2e-54;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTAGTAAAGTCTTCACTGTGGA 60  
 DB 1482 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTAGTAAAGTCTTCACTGTGGA 1541  
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATTAAGTCTTCACTGTGGA 120  
 DB 1542 GCAAGAGCTGGATTTTATGCTTTAGGTGAGGTGATTAAGTCTTCACTGTGGA 1601

QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 180  
Db 1602 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1661  
QY 181 CCAGGGTGCCTAAATATCTG 198  
Db 1662 CCAGGGTGCCTAAATATCTG 1679

RESULT 7  
AAV55038  
ID AAV55038 standard; cDNA; 5232 BP.  
XX  
AC AAV55038;  
XX  
DT 13-NOV-1998 (first entry)  
XX  
DE Human XIAP coding sequence.  
XX  
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
CDS 34..1527  
FT /\*tag= a  
FT /product= XIAP  
XX  
XX WO9835693-A2.  
XX  
XX 20-AUG-1998.  
XX  
XX 13-FEB-1998; 98WO-IB00781.  
XX  
XX 13-FEB-1997; 97US-0800929.  
XX  
XX (UVOOT-) UNIV OTTAWA.

Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
Tsang B;  
WPI: 1998-467164/40.  
P-PSDB: AAW69294.  
Inducing apoptosis in proliferative mammalian cells with inhibitor  
of IAP or NAIP polypeptide - also methods for prognosis based on  
presence of IAP and NAIP, specifically applied to cancers involving  
p53 mutations  
XX  
PS Claim 13; Fig 1; 147pp; English.

This sequence encodes the human XIAP protein, which is an inhibitor of  
apoptosis protein (IAP), and can be used in the method of the invention.  
The method is for enhancing apoptosis in cells from a mammal with  
proliferative disease by treatment with a compound that inhibits  
biological activity of an IAP or NAIP polypeptide. The inhibitory  
compounds are used to treat proliferative diseases, specially cancers of  
ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
liver nasopharynx, thyroid, central nervous system, prostate, colon,  
rectum, cervix or endometrium, particularly to increase their sensitivity  
to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
detected in many cancers and are associated with poor prognosis,  
resistance to chemotherapeutic agents and mutations in p53 (it is  
suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
genes). Transgenic animals are used for testing the effects of antisense  
oligonucleotides and for screening for the inhibitors.

Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;  
Query Match 100.0%; Score 198; DB 19; Length 5232;  
Best Local Similarity 100.0%; Pred No. 2.5e-54;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCCGAGTCTTACTTTTGGGACATGATATCTAGTAAACAGGAGCAGCTT 60  
Db 826 TATGAAGCCGAGTCTTACTTTTGGGACATGATATCTAGTAAACAGGAGCAGCTT 885  
QY 61 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 120  
Db 886 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 945  
QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 180  
Db 946 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1005  
QY 181 CCAGGGTGCCTAAATATCTG 198  
Db 1006 CCAGGGTGCCTAAATATCTG 1023

RESULT 8  
AAD03575  
ID AAD03575 standard; cDNA; 1752 BP.  
XX  
AC AAD03575;  
XX  
DT 19-JUN-2001 (first entry)  
XX  
DE Human IAP-like protein-3 (ILP-3) cDNA.  
XX  
KW Human; inhibitor of apoptosis; IAP-like protein-3; ILP-3;  
KW chromosome 2q12-q14; transforming growth factor beta receptor; TGFbetaR;  
KW c-Jun N-terminal kinase; JNK; gene therapy; osteoarthritis; cytostatic;  
KW hypothyroidism; juvenile nephronophthisis; thrombophilia; cancer;  
KW colorectal cancer; neonatal purpura fulminans; autoimmune disease;  
KW diabetes; multiple sclerosis; neurodegenerative disease;  
KW retinal degeneration; ss.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
CDS 847..1197  
FT /\*tag= a  
FT /product= "Human inhibitor of apoptosis (IAP)-like  
FT protein-3 (hILP-3)"  
XX  
XX WO200123558-A2.  
XX  
XX 05-APR-2001.  
XX  
XX 29-SEP-2000; 2000WO-US26735.  
XX  
XX 30-SEP-1999; 99US-0157169.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Duckett C, Mir SS;  
XX  
XX WPI: 2001-258135/26.  
XX  
XX P-PSDB; AAE00359.

Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with  
transforming growth factor beta receptor modulating activity, and the  
nucleic acids that encode them, useful for treating, e.g. diabetes and  
multiple sclerosis -  
XX  
XX Claim 18; Page 87-88; 108pp; English.  
XX  
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-3  
XX (ILP-3) cDNA. The hILP-3 gene is located on chromosome 2q12-q14.  
XX ILP-3 comprises a spacer region and a ring finger domain. The ILP  
XX interacts with transforming growth factor beta receptor (TGFbetaR) and  
XX modulates TGFbetaR activity. ILP-3 also moderately inhibits ILP-1  
XX mediated c-Jun N-terminal kinase (JNK) activation when co-transfected  
XX with ILP-1. Such activity decreases or prevents apoptosis in a cell.

CC ILP-3 is used in the area of genetic testing for predisposition to  
 CC diseases, such as osteoarthritis, hypothyroidism, juvenile  
 CC nephronophthisis, thrombophilia, colorectal cancer and neonatal purpura  
 CC fulminans owing to an ILP-3 deletion or mutation. The ILP-3 is also used  
 CC in the treatment of diseases associated with abnormal apoptosis such as  
 CC cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and  
 CC neurodegenerative diseases including retinal degeneration. The ILP-3  
 CC gene is also used in gene therapy for treating patients suffering from  
 CC ILP-3 gene deletions or mutations.

XX Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 other;

Query Match 91.1%; Score 180.4; DB 22; Length 1752;  
 Best Local Similarity 94.4%; Pred. No. 9.4e-49;  
 Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGGCTT 60  
 Db 499 TATGAAGCAGGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGGCTT 558  
 Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 120  
 Db 559 TCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 618  
 Qy 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180  
 Db 619 GGGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGATTAATGGCAT 678  
 Qy 181 CCAGGGTGCAAAATATCTG 198  
 Db 679 CCAGGGTGCAAAATATCTG 696

RESULT 9  
 AAT72710  
 ID AAT72710 standard; DNA; 1988 BP.

XX AAT72710;

XX 16-SEP-1997 (first entry)

XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.

XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;  
 XX degenerative disease; infectious disease; autoimmune disease;  
 XX cancer; gene therapy; diagnosis; ss.

XX Mus musculus.

XX Key Location/Qualifiers  
 XX CDS 212..1702  
 XX /\*tag= a

XX WO9723501-A1.

XX 03-JUL-1997.

XX 20-DEC-1996; 96WO-AU00827.

XX 22-DEC-1995; 95AU-0007275.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Vaux DL;

XX WPI; 1997-350966/32.

XX P-PSDB; AAW19745.

XX Isolated protein homologues of viral inhibitors of apoptosis - used  
 XX to modulate apoptosis for treatment of degenerative, infectious or  
 XX autoimmune diseases and cancer

XX Claim 24; Page 44-47; 136pp; English.

XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP  
 CC homologue A (MIHA) (AAW19745), a murine homologue of baculovirus  
 CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse  
 CC liver cDNA library on the basis of homology to Orgyia pseudotsugata  
 CC polyhedrosis virus IAP BIR and RING finger amino acid motifs.  
 CC Animal IAP homologue nucleic acids (see also AAT72711-17) can be used  
 CC to produce polypeptides useful in methods for modulating apoptosis  
 CC in animal cells, specifically for treatment, by inhibition, of  
 CC degenerative and infectious disease or, by promotion, of cancer and  
 CC autoimmune disease, and can be used for gene therapy of these  
 CC diseases.

XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;

Query Match 88.2%; Score 174.6; DB 18; Length 1988;  
 Best Local Similarity 92.9%; Pred. No. 7.7e-47;  
 Matches 183; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGGCTT 60  
 Db 1001 TATGAAGCAGGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGGCTT 1060  
 Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 120  
 Db 1061 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 1120  
 Qy 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180  
 Db 1121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1180  
 Qy 181 CCAGGGTGCAAAATATCT 197  
 Db 1181 CCAGGGTGCAAAATATCT 1197

RESULT 10

AAT70839

ID AAT70839 standard; cDNA; 2100 BP.

XX AAT70839;

XX 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor m-xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
 XX M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
 XX ischaemia; myocardial infarction; stroke;  
 XX reperfusion injury; toxin-induced liver disease; gene therapy;  
 XX diagnosis; ds.

XX Mus sp.

XX Key Location/Qualifiers  
 XX CDS 127..1617  
 XX /\*tag= a

XX WO9706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.

XX 04-AUG-1995; 95US-0511485.

XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;

XX WPI; 1997-154262/14.

XX P-PSDB; AAW19584.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease

XX Claim 11; Page 78-79; 219pp; English.

PS Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and  
 CC hiap-2 genes (AA70836-41) respectively code for a new class of  
 CC mammalian proteins (AAW1981-86) that are inhibitors of apoptosis  
 CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was  
 CC constructed from 12 overlapping clones isolated from a mouse  
 CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic  
 CC library using human xiap cDNA as probe. IAP nucleic acids can be  
 CC used to express IAP polypeptides in cells and animals to inhibit  
 CC apoptosis, and as primers and probes to identify and isolate  
 CC additional IAP genes, as well as in methods for treating diseases  
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).

XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 87.4%; Score 173; DB 18; Length 2100;

Best Local Similarity 92.4%; Pred. No. 2.6e-46;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTACTTTTGGACATGATATCTAGTAAACAGGAGCAGCTT 60

DB 916 TATGAGCAGCGATCTTACTTTTGGACATGATATCTAGTAAACAGGAGCAGCTT 975

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 120

DB 976 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 1035

QY 121 GGAGGCTAACTGATGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 180

DB 1036 GGAGGCTAACTGATGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 1095

QY 181 CCAGGCTGCAAAATATCT 197

DB 1096 CCAGGCTGCAAAATATCT 1112

RESULT 11

ID ABK93872

XX ABK93872 standard; cDNA; 2100 BP.

XX AC ABK93872;

XX DT 26-AUG-2002 (first entry)

XX DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.

XX Mouse; ss; gene; antisense; inhibitor of apoptosis; XIAP1; XIAP2; XIAP;  
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.

XX OS Mus sp.

XX PN WO200226968-A2.

XX PD 04-APR-2002.

XX PF 27-SEP-2001; 2001WO-CA01379.

XX PR 28-SEP-2000; 2000US-0672717.

XX PA (UYOT-) UNIV OTTAWA.

XX PA (AEGE-) AEGERA THERAPEUTICS INC.

XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.

DR P-PSDB; ABG65666..

XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases

XX Disclosure; Fig 4; 135pp; English.

XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP  
 CC cDNA sequence.

XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 87.4%; Score 173; DB 24; Length 2100;

Best Local Similarity 92.4%; Pred. No. 2.6e-46;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTACTTTTGGACATGATATCTAGTAAACAGGAGCAGCTT 60

DB 916 TATGAGCAGCGATCTTACTTTTGGACATGATATCTAGTAAACAGGAGCAGCTT 975

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 120

DB 976 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTCTTCACTGTGGA 1035

QY 121 GGAGGCTAACTGATGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 180

DB 1036 GGAGGCTAACTGATGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 1095

QY 181 CCAGGCTGCAAAATATCT 197

DB 1096 CCAGGCTGCAAAATATCT 1112

RESULT 12

AAV55041

ID AAV55041 standard; cDNA; 2691 BP.

XX AAV55041;

XX AC AAV55041;

XX DT 13-NOV-1998 (first entry)

XX DE Murine XIAP coding sequence.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NATP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.  
 XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT CDS 672..2162

XX FT /\*tag= a

XX FT /product= XIAP

XX PN WO9835693-A2.

XX 20-AUG-1998.  
 XX 13-FEB-1998; 98WO-1800781.  
 PF 13-FEB-1997; 97US-0800929.  
 XX (UVOT-) UNIV OTTAWA.  
 XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX WPI; 1998-467164/40.  
 DR P-PSDB; AAW69297.  
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 XX Claim 13; Fig 4; 147pp; English.  
 XX This sequence encodes the mouse XIAP protein, which is an inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;  
 SQ Query Match 85.88; Score 169.8; DB 19; Length 2691;  
 Best Local Similarity 91.4%; Pred. No. 3.2e-45;  
 Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
 Qy 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGACAGCTT 60  
 Db 1461 TATGAAGCAGCGATCTTTACTTTTGGACATGGACATCTCAGTTAAACAGGACAGCTT 1520  
 Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 120  
 Db 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 1580  
 Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGCCCTTGGGAACACATGCTTAATGGTAT 180  
 Db 1581 GGAGGCTTAAGTGAAGCCAGTGAAGCCCTTGGGAACACATGCTTAATGGTAT 1640  
 Qy 181 CCAGGCTCAAAATATCT 197  
 Db 1641 CCAGGCTCAAAATACCT 1657  
 RESULT 13  
 AAD03582  
 ID AAD03582 standard; cDNA; 711 BP.  
 XX  
 AC AAD03582;  
 XX 19-JUN-2001 (first entry)  
 DT Chimpanzee IAP-like protein-2 (ILP-2) cDNA.  
 DE Inducing apoptosis in proliferative mammalian cells with inhibitor  
 XX of IAP or NAIP polypeptide - also methods for prognosis based on  
 KW presence of IAP and NAIP, specifically applied to cancers involving  
 KW p53 mutations  
 KW Claim 13; Fig 4; 147pp; English.  
 KW This sequence encodes the mouse XIAP protein, which is an inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;  
 SQ Query Match 85.88; Score 169.8; DB 19; Length 2691;  
 Best Local Similarity 91.4%; Pred. No. 3.2e-45;  
 Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
 Qy 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGACAGCTT 60  
 Db 1461 TATGAAGCAGCGATCTTTACTTTTGGACATGGACATCTCAGTTAAACAGGACAGCTT 1520  
 Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 120  
 Db 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 1580  
 Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGCCCTTGGGAACACATGCTTAATGGTAT 180  
 Db 1581 GGAGGCTTAAGTGAAGCCAGTGAAGCCCTTGGGAACACATGCTTAATGGTAT 1640  
 Qy 181 CCAGGCTCAAAATATCT 197  
 Db 1641 CCAGGCTCAAAATACCT 1657

KW c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;  
 KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;  
 KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;  
 KW retinal degeneration; hyperferritinemia-cataract syndrome; cancer;  
 KW autoimmune disease; diabetes; multiple sclerosis; cyclostatic; ss.  
 XX Pan troglodytes.  
 OS  
 XX Key Location/Qualifiers  
 PH CDS 1..711  
 FT /\*cag- a  
 FT /product= "Chimpanzee inhibitor of apoptosis (IAP)-like  
 XX protein-2"  
 PN W0200123568-A2.  
 XX  
 XX 05-APR-2001.  
 XX 29-SEP-2000: 2000WO-US26735.  
 XX 30-SEP-1999: 99US-0157169.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Duckett C, Mir SS;  
 XX WPI; 2001-258135/26.  
 DR P-PSDB; AAE00366.  
 XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with  
 PT transforming growth factor beta receptor modulating activity, and the  
 PT nucleic acids that encode them, useful for treating e.g. diabetes and  
 XX multiple sclerosis -  
 PS Claim 18; Page 99-100; 108pp; English.  
 XX The present sequence is chimpanzee inhibitor of apoptosis (IAP)-like  
 CC protein-2 (ILP-2) cDNA. ILP-2 comprises a single amino-terminal domain  
 CC known as baculovirus IAP repeat (BIR), followed by a spacer region and a  
 CC carboxy-terminal ring finger domain. It interacts with transforming  
 CC growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity.  
 CC It also potentially inhibits apoptosis induced by overexpression of Bax or  
 CC by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)  
 CC activity. ILP-2 is used in the area of genetic testing for predisposition  
 CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,  
 CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer  
 CC and hyperferritinemia-cataract syndrome owing to an ILP-2 deletion or  
 CC mutation. The ILP is also used in the treatment of diseases associated  
 CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,  
 CC diabetes and multiple sclerosis and neurodegenerative diseases including  
 CC retinal degeneration. The ILP-2 gene is also used in gene therapy for  
 CC treating patients suffering from ILP-2 gene deletions or mutations.  
 XX Sequence 711 BP; 235 A; 133 C; 163 G; 180 T; 0 other;  
 SQ Query Match 83.8%; Score 166; DB 22; Length 711;  
 Best Local Similarity 89.9%; Pred. No. 3.4e-44;  
 Matches 178; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 Qy 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGACAGCTT 60  
 Db 10 TATGAAGCCCGGCTCATTACTTTTGGGACATGGATGTTACTTGTAAACAGGACAGCTT 69  
 Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 120  
 Db 70 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 129  
 Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGCCCTTGGGAACACATGCTTAATGGTAT 180  
 Db 130 GGAGGCTTAAGTGAAGCCAGTGAAGCCCTTGGGAACACATGCTTAATGGTAT 189  
 Qy 181 CCAGGCTCAAAATATCTG 198  
 XX

Db 190 CCAGGTGCAAAATATCTG 207

RESULT 14

ABK14677

ID ABK14677 standard; CDNA; 1758 BP.

XX

AC ABK14677;

DT 08-MAY-2002 (first entry)

XX

DE Human inhibitor of apoptosis protein 7 (IAPL7) cDNA.

XX

KW Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;

KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;

KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;

KW cancer; transgenic animal; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 286..1680

FT

FT /\*tag= a

FT /product= "IAPL7 protein"

FT /partial

FT /note= "No start codon shown"

XX

PN WO200210381-A1.

XX

XX 07-FEB-2002.

XX

XX 18-JUL-2001; 2001WO-EP08287.

XX

XX 28-JUL-2000; 2000EP-0116452.

XX

XX (MERE ) MERCK PATENT GMBH.

XX

XX Hentsch B;

XX

XX WPI; 2002-188741/24.

XX

XX P-PSDB; AAU75747.

XX

XX New inhibitor of apoptosis proteins and polynucleotides useful in

XX vaccines for inducing an immune response against hyperproliferative

XX diseases e.g. cancer

XX

XX Claim 5; Page 33-35; 41pp; English.

XX

XX This invention relates to the nucleic acid and protein sequences of a

XX novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences

XX have homology to the IAP (inhibitors of apoptosis) gene family which

XX are thought to inhibit proteins by regulating the anti-apoptotic

XX activity of the V-Rel and NF-kappaB family of transcription factors.

XX The gene for IAPL7 is located on human chromosome 19. The nucleic acids

XX of the invention are useful for screening to identify compounds that

XX stimulate or inhibit the function or level of IAPL7, where the

XX identified compounds are useful for treating hyper-proliferative

XX diseases such as cancer. The protein sequences may also be used to

XX identify membrane bound or soluble receptors of IAPL7 by standard

XX receptor binding techniques. Nucleic acids encoding IAPL7, may be used

XX as hybridisation probes for cDNA and genomic DNA, or as primers for

XX nucleic acid amplification reaction and the primers and probes may also

XX be used to isolate full-length cDNAs and genomic clones encoding IAPL7.

XX The nucleic acid sequences are useful as diagnostic reagents for

XX diagnosing a disease or a susceptibility to a disease by detecting

XX mutations in the associated gene. The nucleic acid sequence is useful

XX for chromosome localisation and tissue expression studies and is also

XX useful for producing transgenic animals. The IAPL7 protein sequence may

XX also be used to generate an anti-IAPL7 antibody which is useful in

XX screening methods for detecting the effect of added compounds on the

XX production of mRNA and protein in cells. The sequences of the invention

XX are also useful as vaccines for inducing an immunological response in a

XX mammal. The present sequence represents the cDNA encoding the human

CC Inhibitor of apoptosis 7 (IAP7) protein of the invention.

XX

SO Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;

Query Match 83.8%; Score 166; DB 24; Length 1758;

Best Local Similarity 89.9%; Pred. No. 4.7e-44;

Matches 178; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCATCTTTTACTTTTGGACATGGATATCTACTAGTTAAACAAGGAGCAGCTT 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 979 TATGAAGCCCGCTCATTTACTTTTGGACATGGATGTTACTCGTTTAAACAAGGAGCAGCTT 1038

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1039 GCAAGAGCTGGATTTATGCTTATAGTCAAGAGGATAAAGTACACTGCTTTTCACTGTGGA 1098

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 GGAGGCTTAAGTGAAGCCCAAGTCAAGACCTTTGGGAACAACATGCTTAATGGTAT 180

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1099 GGAGGCTTAGCCACTGGAAGCCCAAGGAAGATCCTTGGGAACAGCATGCTAAATGGTAT 1158

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 CCAGGTGCAAAATATCTG 198

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1159 CCAGGTGCAAAATATCTG 1176

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15

ABK14678

ID ABK14678 standard; CDNA; 1758 BP.

XX

XX AC ABK14678;

XX

XX 08-MAY-2002 (first entry)

XX

XX Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA #2.

XX

XX Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;

XX antiapoptotic; IAP; apoptosis; V-Rel; NF-kappaB; antibody;

XX chromosome 19; vaccine; gene therapy; hyperproliferative disease;

XX cancer; transgenic animal; ss.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

XX FT CDS 286..687

XX FT /\*tag= a

XX FT /product= "IAPL7 protein"

XX FT /partial

XX FT /note= "This sequence encodes amino acid

XX residues 1-133 of the protein shown in

XX AAU75747. No start codon shown"

XX

XX WO200210381-A1.

XX

XX 07-FEB-2002.

XX

XX 18-JUL-2001; 2001WO-EP08287.

XX

XX 28-JUL-2000; 2000EP-0116452.

XX

XX (MERE ) MERCK PATENT GMBH.

XX

XX Hentsch B;

XX

XX WPI; 2002-188741/24.

XX

XX New inhibitor of apoptosis proteins and polynucleotides useful in

XX vaccines for inducing an immune response against hyperproliferative

XX diseases e.g. cancer

XX

XX Claim 5; Page 36-38; 41pp; English.

XX

XX This invention relates to the nucleic acid and protein sequences of a

XX novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences

XX have homology to the IAP (inhibitors of apoptosis) gene family which

XX are thought to inhibit proteins by regulating the anti-apoptotic

XX activity of the V-Rel and NF-kappaB family of transcription factors.

XX The gene for IAPL7 is located on human chromosome 19. The nucleic acids

XX of the invention are useful for screening to identify compounds that

XX stimulate or inhibit the function or level of IAPL7, where the

XX identified compounds are useful for treating hyper-proliferative

XX diseases such as cancer. The protein sequences may also be used to

XX identify membrane bound or soluble receptors of IAPL7 by standard

XX receptor binding techniques. Nucleic acids encoding IAPL7, may be used

XX as hybridisation probes for cDNA and genomic DNA, or as primers for

XX nucleic acid amplification reaction and the primers and probes may also

XX be used to isolate full-length cDNAs and genomic clones encoding IAPL7.

XX The nucleic acid sequences are useful as diagnostic reagents for

XX diagnosing a disease or a susceptibility to a disease by detecting

XX mutations in the associated gene. The nucleic acid sequence is useful

XX for chromosome localisation and tissue expression studies and is also

XX useful for producing transgenic animals. The IAPL7 protein sequence may

XX also be used to generate an anti-IAPL7 antibody which is useful in

XX screening methods for detecting the effect of added compounds on the

XX production of mRNA and protein in cells. The sequences of the invention

XX are also useful as vaccines for inducing an immunological response in a

XX mammal. The present sequence represents the cDNA encoding the human

Search completed: April 15, 2003, 21:45:29  
Job time : 136.344 secs



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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 24.9219 Seconds  
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Title: US-09-654-743-47  
Perfect score: 198  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A-COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq.\*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	1588	4 US-09-239-867-3	Sequence 3, Appli
2	198	100.0	2540	2 US-08-511-485-3	Sequence 3, Appli
3	198	100.0	2540	3 US-09-392-580-1	Sequence 1, Appli
4	198	100.0	5232	3 US-09-212-971-3	Sequence 3, Appli
5	198	100.0	5232	3 US-08-800-929A-3	Sequence 3, Appli
6	198	100.0	5232	4 US-09-617-053A-3	Sequence 3, Appli
7	173	87.4	2100	2 US-08-511-485-9	Sequence 9, Appli
8	169.8	85.8	2691	3 US-09-212-971-9	Sequence 9, Appli
9	169.8	85.8	2691	3 US-08-800-929A-9	Sequence 9, Appli
10	169.8	85.8	2691	4 US-09-617-053A-9	Sequence 9, Appli
11	164.4	83.0	711	3 US-09-121-979-3	Sequence 3, Appli
12	164.4	83.0	711	4 US-09-332-319-3	Sequence 3, Appli
13	164.4	83.0	1559	4 US-09-239-867-1	Sequence 1, Appli
14	157.8	79.7	152331	3 US-09-128-155-16	Sequence 16, Appli
15	131.4	66.4	176373	3 US-09-128-155-17	Sequence 17, Appli
16	78.6	39.7	2601	4 US-08-569-749-3	Sequence 3, Appli
17	78.6	39.7	2601	5 PCT-US96-12860-3	Sequence 3, Appli
18	78.6	39.7	2676	2 US-08-511-485-5	Sequence 5, Appli
19	78.6	39.7	3076	2 US-09-205-144-1	Sequence 1, Appli
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21	78.6	39.7	6669	3 US-08-800-929A-5	Sequence 5, Appli
22	78.6	39.7	6669	4 US-09-617-053A-5	Sequence 5, Appli
23	74.4	37.6	1435	5 PCT-US95-05922A-1	Sequence 1, Appli
24	74.4	37.6	2580	2 US-08-511-485-7	Sequence 7, Appli
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27	74.4	37.6	3332	2 US-09-205-204-1	Sequence 1, Appli

28 74.4 37.6 3732 3 US-09-212-971-7 Sequence 7, Appli  
29 74.4 37.6 3732 3 US-08-800-929A-7 Sequence 7, Appli  
30 74.4 37.6 3732 4 US-09-617-053A-7 Sequence 7, Appli  
31 71.2 36.0 2862 4 US-08-569-749-13 Sequence 13, Appli  
32 71.2 36.0 2862 5 PCT-US96-12860-13 Sequence 13, Appli  
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34 71.2 36.0 3151 3 US-08-800-929A-13 Sequence 13, Appli  
35 71.2 36.0 3151 4 US-09-617-053A-13 Sequence 13, Appli  
36 70.6 35.7 2676 3 US-09-212-971-11 Sequence 11, Appli  
37 70.6 35.7 2676 3 US-08-800-929A-11 Sequence 11, Appli  
38 70.6 35.7 2676 4 US-09-617-053A-11 Sequence 11, Appli  
39 54.6 27.6 5502 3 US-08-836-134-1 Sequence 1, Appli  
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41 32 16.2 522 4 US-08-998-416-160 Sequence 7, Appli  
c 42 28.4 14.3 736 4 US-09-030-333-7 Sequence 1, Appli  
c 43 28.4 14.3 1824 4 US-09-030-333-1 Sequence 49, Appli  
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c 45 28.4 14.3 1938 4 US-09-295-028-49 Sequence 49, Appli

## ALIGNMENTS

RESULT 1  
US-09-239-867-3  
; Sequence 3, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; TITLE OF INVENTION: MALE FERTILITY  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; PRIOR FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-239-867-3

Query Match 100.0%; Score 198; DB 4; Length 1588;  
Best Local Similarity 100.0%; Pred. No. 1.6e-59;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TATGAAGCAGCGGATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 60  
DB 826 TATGAAGCAGCGGATCTTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTT 885  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 120  
DB 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 945  
QY 121 GGAGGGCTACTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACACATGCTTAATGTTAT 180  
DB 946 GGAGGGCTACTGATTTGGAAGCCAGTGAAGACCCCTTGGGAACACATGCTTAATGTTAT 1005  
QY 181 CCAGGGTGCAAAATATCTG 198  
DB 1006 CCAGGGTGCAAAATATCTG 1023  
RESULT 2  
US-08-511-485-3  
; Sequence 3, Application US/08511485  
; Patent No. 5919912  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen



QY 61 CCAAGAGCTGATTTTATGCTTTAGGTGAAGTGATGAAGTAAAGTCTTTCACTGTGGA 120  
|||||  
Db 886 CCAAGAGCTGATTTTATGCTTTAGGTGAAGTGATGAAGTAAAGTCTTTCACTGTGGA 945  
|||||  
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180  
|||||  
Db 946 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005  
|||||  
QY 181 CCAGGGTGCAAAATATCTG 198  
|||||  
Db 1006 CCAGGGTGCAAAATATCTG 1023  
|||||

## RESULT 5

US-08-800-929A-3  
; Sequence 3, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800.929A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030.590  
; FILING DATE: 14-NOV-1996  
; APPLICATION NUMBER: 60/017.354  
; FILING DATE: 26-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5232 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...5232  
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

Query Match 100.0%; Score 198; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 2.7e-59;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60  
|||||  
Db 826 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885  
|||||  
QY 61 CCAAGAGCTGATTTTATGCTTTAGGTGAAGTGATGAAGTAAAGTCTTTCACTGTGGA 120  
|||||  
Db 886 CCAAGAGCTGATTTTATGCTTTAGGTGAAGTGATGAAGTAAAGTCTTTCACTGTGGA 945  
|||||  
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180  
|||||  
Db 946 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005  
|||||  
QY 181 CCAGGGTGCAAAATATCTG 198  
|||||  
Db 1006 CCAGGGTGCAAAATATCTG 1023  
|||||

## RESULT 6

US-09-617-053A-3  
; Sequence 3, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009003  
; CURRENT APPLICATION NUMBER: US/09/617.053A  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800.929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4623)...(4623)  
; OTHER INFORMATION: n can be any nucleotide  
; NAME/KEY: variation  
; LOCATION: (4622)...(4622)  
; OTHER INFORMATION: n can be any nucleotide  
US-09-617-053A-3

Query Match 100.0%; Score 198; DB 4; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 2.7e-59;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60  
|||||  
Db 826 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885  
|||||  
QY 61 CCAAGAGCTGATTTTATGCTTTAGGTGAAGTGATGAAGTAAAGTCTTTCACTGTGGA 120  
|||||  
Db 886 CCAAGAGCTGATTTTATGCTTTAGGTGAAGTGATGAAGTAAAGTCTTTCACTGTGGA 945  
|||||  
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180  
|||||  
Db 946 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005  
|||||  
QY 181 CCAGGGTGCAAAATATCTG 198  
|||||  
Db 1006 CCAGGGTGCAAAATATCTG 1023  
|||||

## RESULT 7

US-08-511-485-9  
; Sequence 9, Application US/08511485  
; Patent No. 5919912  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/511.485  
; FILING DATE: 04-AUG-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 07540/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2100 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: DNA (genomic)  
US-08-511-485-9

Query Match 87.4%; Score 173; DB 2; Length 2100;  
Best Local Similarity 92.4%; Pred. No. 9.6e-51;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
Qy 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60  
Db 916 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 975  
Qy 61 GCAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 120  
Db 976 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 1035  
Qy 121 GGAGGGCTAACTGATTGGAAGCCAGTCAGACACCTTGGGACACATGCTAAATGGTAT 180  
Db 1036 GGAGGGCTCAGGATTGGAAGCCAGTCAGACACCTTGGGACACATGCTAAATGGTAT 1095  
Qy 181 CCAGGGTGCAAAATATCT 197  
Db 1096 CCAGGGTGCAAAATACCT 1112

## RESULT 8

US-09-212-971-9  
; Sequence 9, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; CURRENT FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2691  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-212-971-9

Query Match 85.8%; Score 169.8; DB 3; Length 2691;  
Best Local Similarity 91.4%; Pred. No. 1.4e-49;  
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
Qy 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60  
Db 1461 TATGAAGCAGCGATCTTTACTTTTGGACATGGACATCTCAGTTAAACAAGGAGCAGCTT 1520  
Qy 61 GCAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 120  
Db 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGA 1580  
Qy 121 GGAGGGCTAACTGATTGGAAGCCAGTCAGACACCTTGGGACACATGCTAAATGGTAT 180  
Db 1581 GGAGGGCTCAGGATTGGAAGCCAGTCAGACACCTTGGGACACATGCTAAATGGTAT 1640  
Qy 181 CCAGGGTGCAAAATATCT 197  
Db 1641 CCAGGGTGCAAAATACCT 1657

## RESULT 9

US-08-800-929A-9  
; Sequence 9, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-800-929A-9

Query Match      85.8%; Score 169.8; DB 3; Length 2691;
Best Local Similarity 91.4%; Pred. No. 1.4e-49;
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACCTCAGTTAAAGGAGCAGCTT 60
Db 1461 TATGAAGCAGCGATCGTTACTTTTGGAACTGGACATCCTCAGTTAAAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGAATAGTCTTTTCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGAATAGTCTTTTCACTGTGGA 1580

QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGACACATGCTTAAATGGTAT 180
Db 1581 GGAGGGCTACGGATTTGAAGCCCAAGTGAAGACCCCTTGGGACACATGCTTAAATGGTAT 1640

QY 181 CCAGGGTGCAAAATATCT 197
Db 1641 CCAGGGTGCAAAATACCT 1657

RESULT 11
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-121-979-3

Query Match      83.0%; Score 164.4; DB 3; Length 711;
Best Local Similarity 89.4%; Pred. No. 5.9e-48;
Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACCTCAGTTAAAGGAGCAGCTT 60
Db 10 TATGAAGCCCGGCTCATTACTTTTGGGACATGGATGTACTCCGTCAACAAAGAGCAGCTT 69

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGAATAGTCTTTTCACTGTGGA 120
Db 70 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGAATAGTCTTTTCACTGTGGA 129

QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGACACATGCTTAAATGGTAT 180
Db 130 GGAGGGCTAGCCACTGGAAGCCCAAGTGAAGATCCTTGGGACACATGCTTAAATGGTAT 189

QY 181 CCAGGGTGCAAAATATCTG 198
Db 190 CCAGGGTGCAAAATATCTG 207

RESULT 12
US-09-332-319-3
; Sequence 3, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
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; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-800-929A-9

Query Match      85.8%; Score 169.8; DB 3; Length 2691;
Best Local Similarity 91.4%; Pred. No. 1.4e-49;
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACCTCAGTTAAAGGAGCAGCTT 60
Db 1461 TATGAAGCAGCGATCGTTACTTTTGGAACTGGACATCCTCAGTTAAAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGAATAGTCTTTTCACTGTGGA 120
Db 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGAATAGTCTTTTCACTGTGGA 1580

QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGACACATGCTTAAATGGTAT 180
Db 1581 GGAGGGCTACGGATTTGAAGCCCAAGTGAAGACCCCTTGGGACACATGCTTAAATGGTAT 1640

QY 181 CCAGGGTGCAAAATATCT 197
Db 1641 CCAGGGTGCAAAATACCT 1657

RESULT 10
US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-617-053A-9
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; CURRENT FILING DATE: 1999-06-14  
; EARLIER APPLICATION NUMBER: 09/121,979  
; EARLIER FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-332-319-3

Query Match! 83.0%; Score 164.4; DB 4; Length 711;  
Best Local Similarity 89.4%; Pred. No. 5.9e-48;  
Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 1 TATGAACGACGGATCTTTACTTTTGGACATGGATATACACTAGTTACACAGGACGCTT 60  
DB 10 TATGAACCGCGGCTCATCTACTTTTGGACATGGATATACACTAGTTACACAGGACGCTT 69  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
DB 70 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 129  
QY 121 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180  
DB 130 GGAGGGCTAGCCAACTGGAAGCCCAAGTGAAGTCTTTGGGAACAACATGCTAAATGGTAT 189  
QY 181 CCAGGGTGCAAAATATCTG 198  
DB 190 CCAGGGTGCAAAATATCTG 207

RESULT 13  
US-09-239-867-1  
; Sequence 1, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1559  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1559)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-239-867-1

Query Match 83.0%; Score 164.4; DB 4; Length 1559;  
Best Local Similarity 89.4%; Pred. No. 8.4e-48;  
Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 1 TATGAACGACGGATCTTTACTTTTGGACATGGATATACACTAGTTACACAGGACGCTT 60  
DB 800 TATGAACCGCGGCTCATCTACTTTTGGACATGGATATACACTAGTTACACAGGACGCTT 859  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
DB 860 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 919  
QY 121 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180  
DB 920 GGAGGGCTAGCCAACTGGAAGCCCAAGTGAAGTCTTTGGGAACAACATGCTAAATGGTAT 979

QY 181 CCAGGGTGCAAAATATCTG 198  
DB 980 CCAGGGTGCAAAATATCTG 997  
RESULT 14  
US-09-128-155-16/c  
; Sequence 16, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 152331  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(152331)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-16

Query Match 79.7%; Score 157.8; DB 3; Length 152331;  
Best Local Similarity 90.4%; Pred. No. 1.2e-44;  
Matches 179; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
QY 1 TATGAACGACGGATCTTTACTTTTGGACATGGATATACACTAGTTACACAGGACGCTT 60  
DB 3298 TATGAACGATGGATCATCTACTTTTGGGATGGATATATTCAGTTACACAGGACGCTT 3239  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
DB 3238 TCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 3179  
QY 121 GGAGGGCTAACTGATTTGAAGCCCAAGTGAAGCCCTTGGGAACAACATGCTAAATGGTAT 180  
DB 3178 GGGGGCTAACTGATTTGGGACCCCAAGTGAAGTCTTTGGGACCAACATTAATAATGGGAT 3120  
QY 181 CCAGGGTGCAAAATATCTG 198  
DB 3119 CCAGGGTGCAAAATATCTG 3102

RESULT 15  
US-09-128-155-17  
; Sequence 17, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 176373  
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match      66.4%; Score 131.4; DB 3; Length 176373;
Best Local Similarity 95.7%; Pred. No. 2.1e-35;
Matches 135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 CTGCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGT 117
Db 12549 CTTTCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACTGT 12608

QY 118 GGAGGAGGGCTACTGATTGGAGCCCGAGTCAAGACCCCTTGGGAACAACATGCTAAATGG 177
Db 12609 GGAGGAGGGCTACTGATTGGAGCCCGAGTCAAGACCCCTTGGGAACAACATGATAAATGG 12668

QY 178 TATCCAGGGTGCAAAATATCTG 198
Db 12669 CATCCAGGGTGTAATAATCTG 12689
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Search completed: April 16, 2003, 00:58:14  
Job time : 66.9219 secs





```
RESULT 2
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match          100.0%; Score 198; DB 9; Length 2540;
Best Local Similarity 100.0%; Pred. No. 7.7e-56;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATCTAGTTAAACAAGGAGCGCTT 60
    |||||||
Db 826 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATCTAGTTAAACAAGGAGCGCTT 885

Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 120
    |||||||
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 945

Qy 121 GGAGGCTAACTGATTTGGAAGCCCGAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 180
    |||||||
Db 946 GGAGGCTAACTGATTTGGAAGCCCGAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1005

Qy 181 CCAGGGTGCATAATATCTG 198
    |||||||
Db 1006 CCAGGGTGCATAATATCTG 1023

RESULT 3
US-09-974-592-3
; Sequence 3, Application US/09074592
; Patent No. US2002012012A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974.592
```

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; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match          100.0%; Score 198; DB 10; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATCTAGTTAAACAAGGAGCGCTT 60
    |||||||
Db 826 TATGAAGCAGCGATCTTTACCTTTGGGACATGGATATCTAGTTAAACAAGGAGCGCTT 885

Qy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 120
    |||||||
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 945

Qy 121 GGAGGCTAACTGATTTGGAAGCCCGAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 180
    |||||||
Db 946 GGAGGCTAACTGATTTGGAAGCCCGAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1005

Qy 181 CCAGGGTGCATAATATCTG 198
    |||||||
Db 1006 CCAGGGTGCATAATATCTG 1023

RESULT 4
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match          87.4%; Score 173; DB 9; Length 2100;
Best Local Similarity 92.4%; Pred. No. 1.5e-47;
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Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTGGGACATGGATATACTCAGTTAAAGAGGAGCAGCTT 60  
|||||  
DB 916 TATGAAGCAGGATCTTTACTTTGGGACATGGATATACTCAGTTAAAGAGGAGCAGCTT 975  
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120  
|||||  
DB 976 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 1035  
|||||

QY 121 GGAGGCTPAAGTGAAGGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180  
|||||  
DB 1036 GGAGGCTPAAGTGAAGGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 1095  
|||||

QY 181 CCAGGTCGCAATATCT 197  
|||||  
DB 1096 CCAGGTCGCAATATCT 1112  
|||||

## RESULT 5

US-09-974-592-9

; Sequence 9, Application US/09974592

; Patent No. US20020120121A1

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 07891/009004

; CURRENT APPLICATION NUMBER: US/09/974.592

; CURRENT FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: US 09/617,053

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/800,929

; PRIOR FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2691

; TYPE: DNA

; ORGANISM: Mus musculus

; US-09-974-592-9

Query Match

Best Local Similarity 85.8%; Score 169.8; DB 10; Length 2691;

Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTTACTTTGGGACATGGATATACTCAGTTAAAGAGGAGCAGCTT 60

DB 1461 TATGAAGCAGGATCTTTACTTTGGGACATGGATATACTCAGTTAAAGAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120

DB 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 1580

QY 121 GGAGGCTPAAGTGAAGGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180

DB 1581 GGAGGCTPAAGTGAAGGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 1640

QY 181 CCAGGTCGCAATATCT 197

DB 1641 CCAGGTCGCAATATCT 1657

RESULT 6

US-10-095-407-16/c

; Sequence 16, Application US/10095407

; Patent No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yaog

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 16

LENGTH: 152331

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)-(152331)

OTHER INFORMATION: n = A,T,C or G

US-10-095-407-16

Query Match

Best Local Similarity 79.7%; Score 157.8; DB 9; Length 152331;

Matches 179; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1 TATGAAGCAGGATCTTTACTTTGGGACATGGATATACTCAGTTAAAGAGGAGCAGCTT 60

DB 3298 TATGAAGCAGGATCTTTACTTTGGGATGTGGATATATTTCAGTTAAAGAGGAGCAGCTT 3239

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120

DB 3238 TCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 3179

QY 121 GGAGGCTPAAGTGAAGGCCAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180

DB 3178 GGGGGCTAAGTGAAGTGAAGACCCCGAA-AACCTTGGGACAAACATGCTAAATGGTAT 3120

QY 181 CCAGGTCGCAATATCTG 198

DB 3119 CCAGGTCGCAATATCTG 3102

## RESULT 7

US-10-095-407-17

; Sequence 17, Application US/10095407

; Patent No. US20020164330A1

; GENERAL INFORMATION:

; APPLICANT: Pan, Yaog

; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; FILE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/10/095,407

; CURRENT FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/091,650

; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: US 60/054,646

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 176373

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)-(176373)

; OTHER INFORMATION: n = A,T,C or G

US-10-095-407-17

## Query Match

Best Local Similarity

US-10-095-407-16/c

; Sequence 16, Application US/10095407

; Patent No. US20020164330A1

Query Match

Best Local Similarity

US-10-095-407-17

; Sequence 17, Application US/10095407

; Patent No. US20020164330A1



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; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 39.7%; Score 78.6; DB 10; Length 3076;
Best Local Similarity 68.8%; Pred. No. 4.6e-16;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAACAGGAGCAGCTTGCAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGT 101
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1534 AGTTAATCCTGACGCTTGCAGCTTGCAGTCCGGGTTTTATTATGGGTAAACAGTGATGT 1593

QY 102 AAAGTCTTTACTGTGGAGGAGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGA 161
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1594 CAAATGCTTTCTGTGATGGTGGACTCAGGTCTGGGAATCGGAGATGATCCATGGT 1653

QY 162 ACAACATGTAATGATCCAGGTGCAAAATATCTG 198
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1654 TCACATGCCAAGTGTTCACAGGTGTGAGTACTTG 1690

RESULT 11
US-09-974-592-5
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

Query Match 39.7%; Score 78.6; DB 10; Length 6669;
Best Local Similarity 68.8%; Pred. No. 6.6e-16;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAACAGGAGCAGCTTGCAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGT 101
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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DB 5030 AGTTAATCCTGACGAGCTTGCAGAGTCCGGGTTTTATTATGTTGGTAAACAGTGATGT 5089
QY 102 AAAGTCTTTACTGTGGAGGAGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGA 161
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 5090 CAAATGCTTTCTGTGATGGTGGACTCAGGTCTGGGAATCGGAGATGATCCATGGT 5149
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 162 ACAACATGTAATGATCCAGGTGCAAAATATCTG 198
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 5150 TCAACATGCCAAGTGTTCACAGGTGTGAGTACTTG 5186
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 12
US-09-201-936-7
; Sequence 7, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match 37.6%; Score 74.4; DB 9; Length 2580;
Best Local Similarity 62.2%; Pred. No. 1.1e-14;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 11 GGATCTTTACTTTTGGGACATGGATATCTCAGTTAAACAGGAGCAGCTTGCAGAGCTG 70
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1058 GAACATTTATGTACTGGCCATCTAGTGTTCAGCTTCCAGCTTGAGAGCTTGCAGAGTCTG 1117
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 71 GATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGGCTAA 130
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1118 GTTTTATTTATGTGGTCCGAATGATGATGTCAATGCTTTGTTGTGATGGTGGCTTGA 1177
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 131 CTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGCTATCCAGGGTGA 190
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1178 GGTGTGGGAATCTGGAGATGATCCATGGGTGGTAGAACATGCCAAGTGTTCACAGGTGTG 1237
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 191 AATATCTG 198
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1238 AGTCTTG 1245
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 13
US-09-880-107-3354
; Sequence 3354, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.

```

```

; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880.107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3354
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U37547
; US-09-880-107-3354

Query Match      37.6%; Score 74.4; DB 10; Length 3532;
Best Local Similarity 62.2%; Pred. No. 1.2e-14;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 11 GGATCTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTTGCAGAGCTG 70
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1980 GAACATTTATGTTAGTGGCCATCTAGTGTCCAGTTCAGCCTGAGCAGCTTGCAGAGCTG 2039

QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAA 130
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2040 GTTTTATATGTTGGTGGCGCAATGATGTCAAATGCTTTTGTGTGATGGTGGCTTGA 2099

QY 131 CTGATTGGAAGCCCGAGTGAAGACCCCTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2100 GGTGTTGGATCTCGAGATGATCCATGGGTAGACATGCCAAGTGGTTCACAGGTGTG 2159

QY 191 AATATCTG 198
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2160 AGTTCCTG 2167

RESULT 14
US-09-974-592-7
; Sequence 7, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974.592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-974-592-7

Query Match      37.6%; Score 74.4; DB 10; Length 3732;
Best Local Similarity 62.2%; Pred. No. 1.3e-14;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 11 GGATCTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTTGCAGAGCTG 70
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1578 GGACATTTCTGTAAGTGGCCACCTAGTGTCTCCTGTTCAAGCCGAGCAGCTTGCAGAGCTG 1637

QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAA 130
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1638 GATTCATTACGTCGCAATGATGATGTCAGTGTCTTTGTGTGATGGTGGCTTGA 1697

QY 131 CTGATTGGAAGCCCGAGTGAAGACCCCTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1698 GATGTTGGGAACCTGGAGATGATCCCTGGATAGAACACACCCCAATGGTTCACAGGTGTG 1757

QY 191 AATATCTG 198
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1758 AGTTCCTG 1765

Search completed: April 16, 2003, 01:03:10
Job time : 90.6094 secs
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```

QY 11 GGATCTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTTGCAGAGCTG 70
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DB 2200 GAACATTTATGTTAGTGGCCATCTAGTGTCCAGTTCAGCCTGAGCAGCTTGCAGAGCTG 2259

QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAA 130
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2260 GTTTTATATGTTGGTGGCGCAATGATGATGTCAAATGCTTTTGTGTGATGGTGGCTTGA 2319

QY 131 CTGATTGGAAGCCCGAGTGAAGACCCCTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2320 GGTGTTGGATCTCGAGATGATCCATGGGTAGACATGCCAAGTGGTTCACAGGTGTG 2379

QY 191 AATATCTG 198
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2380 AGTTCCTG 2387

RESULT 15
US-09-974-592-13
; Sequence 13, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974.592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-974-592-13

Query Match      36.0%; Score 71.2; DB 10; Length 3151;
Best Local Similarity 61.2%; Pred. No. 1.3e-13;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 11 GGATCTTACTTTTGGGACATGATATCTCAGTTAAACAAGGAGCAGCTTGCAGAGCTG 70
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1578 GGACATTTCTGTAAGTGGCCACCTAGTGTCTCCTGTTCAAGCCGAGCAGCTTGCAGAGCTG 1637

QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTCACCTGTGGAGGAGGCTAA 130
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1638 GATTCATTACGTCGCAATGATGATGTCAGTGTCTTTGTGTGATGGTGGCTTGA 1697

QY 131 CTGATTGGAAGCCCGAGTGAAGACCCCTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1698 GATGTTGGGAACCTGGAGATGATCCCTGGATAGAACACACCCCAATGGTTCACAGGTGTG 1757

QY 191 AATATCTG 198
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1758 AGTTCCTG 1765

Search completed: April 16, 2003, 01:03:10
Job time : 90.6094 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; search time 947.375 seconds

(without alignments)  
3384.833 Million cell updates/sec

Title: US-09-654-743-47

Perfect score: 198

Sequence: 1 tatgaagcaggtatcttacc.....atccagggtgcaatatctg 198

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_etc:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	157.4	79.5	628	9	AI573382
2	114	57.6	1177	14	BM805359
3	112	56.6	536	9	AU123207
4	104.4	52.7	716	10	AV706807
5	100.2	50.6	318	12	BF559610
6	99	50.0	617	10	BB663325

7	94.4	47.7	504	10	BB650856
8	91.6	46.3	566	13	BM220130
9	91.6	46.3	584	14	BO552032
10	87	43.9	420	17	AQ011995
11	78.6	39.7	341	10	AW375598
12	78.6	39.7	354	10	AW375594
13	78.6	39.7	402	10	AW846507
14	78.6	39.7	531	10	AW375599
15	78.6	39.7	532	10	AW846425
16	78.6	39.7	546	10	AW846421
17	78.6	39.7	571	10	AW375649
18	78.6	39.7	582	10	AW375648
19	78.6	39.7	590	10	BE268377
20	78.6	39.7	621	10	AW375648
21	78.6	39.7	680	10	AW375625
22	78.6	39.7	886	14	BO652590
23	78.4	39.6	289	10	BE506790
24	74.4	37.6	441	13	BM312708
25	74.4	37.6	563	9	AA702174
26	74.4	37.6	652	10	AV704923
27	74.4	37.6	851	13	BI253303
28	74.4	37.6	896	14	BO439248
29	74.4	37.6	354	9	AA34707
30	73.4	37.1	567	13	BI961039
31	73.4	37.1	889	14	BO720079
32	71.2	36.0	298	12	BF016190
33	71.2	36.0	780	13	BI771720
34	70.6	35.7	333	12	BE847058
35	70.6	35.7	385	12	BE851680
36	70.6	35.7	557	9	AA197349
37	70	35.4	506	13	BM126304
38	69.6	35.2	395	9	AI552965
39	69.4	35.1	302	14	R83677
40	68.5	34.6	673	13	BJ045197
41	68	34.3	286	9	AA473594
42	66.6	33.6	592	13	BJ059822
43	65.4	33.0	423	12	BF325539
44	65	32.8	584	10	AW375608
45	65	32.8	645	10	AW375611

#### ALIGNMENTS

RESULT 1  
AI573382/c  
LOCUS  
DEFINITION  
mm83e12.x1 Stratagene mouse tcell 937311 Mus musculus cDNA clone  
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ; mRNA sequence.  
ACCESSION  
AI573382  
VERSION  
AI573382.1 GI:4536756  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 628)  
Mamma.M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, P., Person  
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter  
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
TITLE  
The WashU-NCI Mouse EST Project 1999  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand

BB650856 BB650856  
BM220130 C0935E08-  
BO552032 H4013A06-  
AQ011995 HS\_2190.A  
AW375598 QVO-CT017  
AW375594 QVO-CT017  
AW846507 QVO-CT017  
AW375599 QVO-CT017  
AW846425 QVO-CT017  
AW846421 QVO-CT017  
AW375649 QVO-CT017  
AW846337 QVO-CT017  
BE268377 601124994  
AW375648 QVO-CT017  
AW375625 QVO-CT017  
BO652590 AGENCOURT  
BE506790 dB87908.Y  
BM312708 Iq78a10.Y  
AA702174 z191908.S  
AV704923 AV704923  
BO439248 AGENCOURT  
BA34707 EST63004  
BI961039 MONOL\_5\_C  
BO720079 AGENCOURT  
BF016190 UY32A08.Y  
BI771720 603058472  
BE847058 uw23A06.Y  
BE851680 uw99007.Y  
AA197349 mu21C08.F  
BM126304 IF04609.Y  
AI552965 vg63h10.Y  
R83677 vp16f10.r1  
BJ045197 BJ045197  
AA473594 vg63h10.F  
BJ059822 BJ059822  
BF325539 C40-AN000  
AW375608 QVO-CT017  
AW375611 QVO-CT017

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FEATURES
source
High quality sequence stop: 440.
Location/Qualifiers
1..628
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_image="550702"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site:1:
ECORI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAACTGGCAGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
BASE COUNT 163 a 137 c 115 g 211 t 2 others
ORIGIN
Query Match 79.5%; Score 157.4; DB 9; Length 628;
Best Local Similarity 90.4%; Pred. No. 4e-41; 18; Indels 1; Gaps 1;
Matches 178; Conservative 0; Mismatches 0;

QY 1 TATGAAGCAGGATCTTTTCTTTGGGACATGATATACCTAGCTTAAACAAGGAGCAGCTT 60
|||||
Db 604 TATGAAGCAGGATCTTTTCTTTGGGACATGATATACCTAGCTTAAACAAGGAGCAGCTT 545
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGGAAGGTGATAAAGTAAAGTCTTTCTACTGTGGA 120
|||||
Db 544 GCAAGAGCT-GATTTATGCTTTTAGTGGAAGGTGATAAAGTAAAGTCTTTCTACTGTGGA 486
|||||

QY 121 GGAGGCTAACTGATTTGGAGCCAGTGAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 485 GGAGGCTAACGATTTGGAGCCAGTGAGACCCCTTGGGAACAACATGCTAAATGGTAT 426
|||||

QY 181 CCAGGTGCAAAATATCT 197
|||||
Db 425 NCAGGTGCAAAATATCT 409
|||||

RESULT 2
BM805359
LOCUS
DEFINITION 1177 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6499731 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5728685
5', mRNA sequence.
ACCESSION BM805359
VERSION BM805359.1 GI:19122182
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1177)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@femail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12724 row: m column: 06
High quality sequence stop: 409.
Location/Qualifiers
1..1177
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5728685"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
FEATURES
source

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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: EcoRV
(destroyed); Site:2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 284 a 362 c 221 g 310 t
ORIGIN
Query Match 57.6%; Score 114; DB 14; Length 1177;
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAAGCCC 144
|||||
Db 142 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAAGCCC 201
|||||

QY 145 AGTGAAGACCTTGGGAACAACATGCTAAATGATATCCAGGGTGCAATATCTG 198
|||||
Db 202 AGTGAAGACCTTGGGAACAACATGCTAAATGATATCCAGGGTGCAATATCTG 255
|||||

RESULT 3
AUI23207 536 bp mRNA linear EST 01-AUG-2002
LOCUS AUI23207 NT2RM1 Homo sapiens CDNA clone NT2RM1000921 5', mRNA
sequence.
ACCESSION AUI23207
VERSION AUI23207.1 GI:10947923
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 536)
Ota.T., Nishikawa.T., Suzuki.Y., Kawai.Y., Ishii.S., Saito.K.,
Nakamura.Y., Nagai.T., Sugano.S. and Isogai.T.
HRI human CDNA project (Ota.T., Nishikawa.T., Suzuki.Y., Kawai.Y.,
Ishii.S., Saito.K., Nakamura.Y., Nagai.T., Sugano.S., Isogai.T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
1..536
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="NT2RM1000921"
/clone_lib="NT2RM1"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"
BASE COUNT 172 a 105 c 126 g 124 t 9 others
ORIGIN
Query Match 56.8%; Score 112; DB 9; Length 536;
Best Local Similarity 98.2%; Pred. No. 4.1e-26;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 85 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAAGCCC 144
|||||

```

Db 99 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAGGCC 158

QY 145 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGGCAATATCTG 198

Db 159 AGTGAANACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGGCAATATCTG 212

RESULT 4

AV706807 716 bp mRNA linear EST 09-OCT-2000

DEFINITION AV706807 ADB Homo sapiens cDNA clone ADBCOF01 5', mRNA sequence.

ACCESSION JAV706807

VERSION AV706807.1 GI:10724085

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 716)

Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.

TITLE Homo sapiens cDNA ADB clones

JOURNAL Unpublished (2000)

COMMENT Contact: Zequang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzeqhc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES

Source Location/Qualifiers

1..716

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="ADBCOF01"

/clone\_lib="ADB"

/tissue\_type="Adrenal gland"

/dev\_stage="Adult"

/lab\_host="SOLR"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 207 a 148 c 193 g 163 t 5 others

ORIGIN

Query Match 52.7%; Score 104.4; DB 10; Length 716;  
Best Local Similarity 94.7%; Pred. No. 1.6e-23; Indels 0; Gaps 0;  
Matches 108; Conservative 0; Mismatches 6;

QY 85 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAGGCC 144

Db 156 GGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAGGCC 215

QY 145 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGGCAATATCTG 198

Db 216 AGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTAAAGAACTACTG 269

RESULT 5

BF659610/c 318 bp mRNA linear EST 29-DEC-2000

LOCUS uz88912.x1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3676174 3'

DEFINITION similar to SW:IAIP3\_MOUSE Q60989 INHIBITOR OF APOPTOSIS PROTEIN 3 ; mRNA sequence.

ACCESSION BF659610

VERSION BF659610.1 GI:11924744

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 318)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

MGI:1436942

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco

High quality sequence stop: 226.

FEATURES

Source Location/Qualifiers

1..318

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:3676174"

/clone\_lib="NCI\_CGAP\_Lu29"

/tissue\_type="spontaneous tumor, metastatic to mammary. Stem cell origin"

/lab\_host="DH10B"

/note="Organ: lung; Vector: pCMV-Sport6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 73 a 78 c 53 g 114 t

ORIGIN

Query Match 50.6%; Score 100.2; DB 12; Length 318;  
Best Local Similarity 92.9%; Pred. No. 2.4e-22; Indels 0; Gaps 0;  
Matches 105; Conservative 0; Mismatches 8;

QY 53 AGCAGCTTGCAGAGCTGGATTTATGCTTAGGTGAAGGTGATATAAGTAAAGTCTTTC 112

Db 317 AGCAGCTTGCAGAGCTGGATTTATGCTTAGGTGAAGGTGATATAAGTAAAGTCTTTC 258

QY 113 ACTGTGGAGGAGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGACAA 165

Db 257 ACTGTGGAGGAGGCTCTCGGATTGGAAGCCAGTGAAGACCCCTTGGGACAA 205

RESULT 6

BB663325 617 bp mRNA linear EST 26-OCT-2001

LOCUS BB663325 RIKEN full-length enriched, 15 days embryo head Mus

DEFINITION musculus cDNA clone D930039G22 5', mRNA sequence.

ACCESSION BB663325

VERSION BB663325.1 GI:16497079

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 617)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koyas, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic



GGGAACCCAGTGAAGACCTTGGGAACAACATGCTAAATGGTATCCAGGTGCAATA 194

FEATURES  
source

5'-pGACCTAGTCTCTAGACGGCGAGCGGCCGCCCTTTTTTTTTT-3') from total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal-I, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal-I-5. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal-I and NotI enzymes and cloned into SalI/NotI site of pSPORI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed

BASE COUNT	183 a	123 c	84 g	176 t	
ORIGIN					
					Dy ruan Piso (wA).
Query Watch					46.3%; Score 91.6; DB 13; Length 566;
Best Local Similarity					91.5%; Pred. No. 2.5e-19;
Matches 97; Conservative					0; Mismatches 9; Indels 0; Gaps 0;
QY	82	TTAGGTGAAGGTGATAAAGTAAAGTGCTTTCTACTGTGGAGAGGGGTAACTGATTGGAA	141		
Db	260	TTAGGTGAAGCCGATAAAGTGAAGTGTCTTCACTGTGGAGAGGGGTCAAGGATTGGAA	201		

	BQ52032	584 bp	mRNA	linear	EST 20-JUN-2002
RESULT 9	BQ52032/c				
LOCUS	H4013A06-3	NIA Mouse	7.4K cDNA Clone Set	Mus musculus	cDNA clone
DEFINITION	H4013A06 3'	mRNA sequence.			

National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgsun.grc.nia.nih.gov  
 This clone set has been freely distributed to the community. Please  
 visit [http://lgsun.grc.nia.nih.gov/cDNA/NIA\\_7\\_4k.html](http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html) for details.  
 Plate: H4013 row: A column: 06  
 Seq primer: -21M13 Forward  
 High quality sequence stop: 584  
 POLYA=Yes.

FEATURES	Location/Qualifiers
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/db_xref="taxon:10090"
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/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/notes="vector: pSP0rt1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."
BASE COUNT 189 a 125 c 86 g 184 t
ORIGIN
Query Match 46.3%; Score 91.6; DB 14; Length 584;
Best Local Similarity 91.5%; Pred. No. 2.5e-19;
Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 82 TTAGTGAAGGTATTAAGTAAAGTCTTCACTGTCGAGGAGGCTCACTGTTGGAG 141
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DB 260 TTAGTGAAGGCGATAAAGTGAAGTCTTCACTGTCGAGGAGGCTCACTGTTGGAG 201
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QY 142 CCCAGTGAAGCCCTTGGCAACATGCTAAATGGTATCCAGGCT 187
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DB 200 CCAAGTGAAGCCCTTGGCAACATGCTAAATGGTATCCAGGCT 155
|||||

RESULT 10
A0011995/c
LOCUS
DEFINITION HS_2190_AL_MR_G12 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2190 Col=23 Row=M, DNA sequence.
ACCESSION A0011995
VERSION A0011995.1 GI:3171671
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 420)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 9380589
COMMENT Contact: Mahairas GS, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2190 row: M column: 23
Class: BAC ends
High quality sequence stop: 420.
Location/Qualifiers:
1..420
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2190 Col=23 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/notes="Organ: sperm; Vector: pBel0BAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 98 a 93 c 73 g 156 t
ORIGIN
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Best Local Similarity 94.7%; Pred. No. 6.8e-18;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 104 AGTCTTTCACTGCGAGGAGGCTTAAGTATTGGAAGCCAGTGAAGACCTTTGGGAAAC 163
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DB 420 AGTCTTTCACTGCGAGGAGGCTTAAGTATTGGAAGCCAGTGAAGACCTTTGGGAAAC 361
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QY 164 AACATGCTAAATGGTATCCAGGCTCAAAATATCTG 198
|||||
DB 360 AACATGATAAATGGCATCCAGGCTGTAATATCTG 326
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RESULT 11
AW375598
LOCUS
DEFINITION QV0-CT0179-300999-024-f08 CT0179 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW375598
VERSION AW375598.1 GI:6880161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 341)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l-QV0&t2-QV0-CT0179-
300999-024-f08&t3-1999-09-30&t4-1)
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High quality sequence start: 15
High quality sequence stop: 341.
Location/Qualifiers:
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/db_xref="taxon:9606"
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/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 91 a 70 c 83 g 97 t
ORIGIN
Query Match 39.7%; Score 78.6; DB 10; Length 341;
Best Local Similarity 68.8%; Pred. No. 3.7e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGAGCAGCTTGCAGAGCTGGATTTATCTTTAGTGAAGTGTAAGT 101
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DB 80 AGTTAACTCTGAGCAGCTTGCAGAGTCCGGGTTTTATTATGTGGTAAACAGTGATGT 139
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QY 102 AAGTGTCTTCACTGTCGAGGAGGCTAACTCATTTGGAGCCCACTGAAGACCCCTTGGGA 161
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DB 140 CAATGCTTTGCTGTATGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCAATGGT 199
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QY 162 ACAACATGCTAAATGGTATCCAGGCTGCAAAATATCTG 198
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DB 200 TCACATGCCAAGTGGTTTCCCAAGCTGTGAGTACTTG 236
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RESULT 12

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AW375599	AW375599	531 bp	linear	EST 04-FEB-2000		
LOCUS	QVO-CT0179-300999-024-g04	CT0179	Homo sapiens	cDNA, mRNA sequence.		
DEFINITION						
ACCESSION	AW375599					
VERSION	AW375599.1	GI:6880162				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 531)					
AUTHORS	HCGP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a>					
TITLE	The FAPESP/LICR Human Cancer Genome Project					

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-CT0179-  
300999-024-g04&t3=1999-09-30&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 16  
High quality sequence stop: 531.

FEATURES  
source

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/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: Sma1; Site\_2:  
Sma1; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

BASE COUNT 158 a 108 c 121 g 144 t

Query Match 39.7%; Score 78.6; DB 10; Length 531;  
Best Local Similarity 68.8%; Pred. No. 4.8e-15;  
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
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Db 139 AGTTAACTCTGAGCAGCTTGCAGAGCTGGGTTTATTTATGTTGGTAAACAGTGATGCT 198  
QY 102 AAGTGCCTTCTACTGTGGAGGGGCTAACTGATTTGGAAGCCAGTGAAGACCCCTTGGGA 161  
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Db 199 CAAATGCTTTGCTGTGATGGTGGAGCTCAGGTGTTGGGAATCTGGAGATGCCATGGGT 258  
QY 162 ACAACATGCTAAATGCTATCCAGGGTGCAAAATATCTG 198  
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Db 259 TCAACATGCCAGTGGTTTCCAGGTGTCAGTACTTG 295

## RESULT 15

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DEFINITION QV0-CT0179-070300-143-d09 CT0179 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW846425  
VERSION AW846425.1 GI:7941942  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 532)  
Dias Neto,E., Garcia Correia,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balg,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

## TITLE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL 20202663  
MEDLINE  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-CT0179-070  
300-143-d09&t3=2000-03-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 4  
High quality sequence stop: 531.

FEATURES  
source

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/db\_xref="taxon:9606"  
/clone\_lib="CT0179"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: Sma1; Site\_2:  
Sma1; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

BASE COUNT 160 a 107 c 122 g 143 t

Query Match 39.7%; Score 78.6; DB 10; Length 532;  
Best Local Similarity 68.8%; Pred. No. 4.8e-15;  
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
QY 42 AGTTAAAGGAGGACGCTTGCAGAGCTGGATTATGCTTTAGTGAAGGTGATAAAGT 101  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 96 AGTTAACTCTGAGCAGCTTGCAGAGCTGGGTTTATTTATGTTGGTAAACAGTGATGCT 155  
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Db 216 TCAACATGCCAGTGGTTTCCAGGTGTCAGTACTTG 252

Search completed: April 16, 2003, 00:54:57  
Job time : 950.375 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: April 15, 2003, 19:40:42 ; Search time 1031.86 seconds  
(without alignments)  
5753.635 Million cell updates/sec

Title: US-09-654-743-49  
Perfect score: 204  
Sequence: 1 gagttaataagattaaaac.....ccccaaattgcagattattac 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.jnu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
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- 35: em.htg\_rtd.\*
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- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	204	100.0	2100	6	AX412124	AX412124 Sequence
2	204	100.0	2691	6	AR106400	AR106400 Sequence
3	204	100.0	2691	6	AR116702	AR116702 Sequence
4	204	100.0	2691	10	MM088990	U88990 Mus musculus
5	202.4	99.2	1988	10	MMU36842	U36842 Mus musculus
6	189.6	92.9	2032	10	AF304333	AF304333 Rattus no
7	189.6	92.9	2468	10	AB033366	AB033366 Rattus no
8	189.6	92.9	3032	10	AF304334	AF304334 Rattus no
9	188	92.2	1491	10	AF183429	AF183429 Rattus no
10	172	84.3	1659	6	E31042	E31042 Method for
11	172	84.3	1659	9	HSU32974	U32974 Human TAP-1
12	172	84.3	2086	9	BC032729	BC032729 Homo sapi
13	172	84.3	2404	6	AX429575	AX429575 Sequence
14	172	84.3	2540	6	AR103281	AR103281 Sequence
15	172	84.3	2540	6	AX412118	AX412118 Sequence
16	172	84.3	2540	9	HSU45880	U45880 Human X-lin
17	172	84.3	3000	6	AX412131	AX412131 Sequence
18	172	84.3	5232	6	AR106397	AR106397 Sequence
19	172	84.3	5232	6	AR116699	AR116699 Sequence
20	172	84.3	13391	9	HSU331561	AL121601 Human DNA
21	172	84.3	201197	2	HS424012	282207 Homo sapien
C 22	134.4	65.9	187568	9	AP002967	AP002967 Homo sapi
23	127.8	62.6	7990	6	AX281265	AX281265 Sequence
24	127.8	62.6	7990	6	AX345060	AX345060 Sequence
C 25	110.2	54.0	7990	6	AX381266	AX381266 Sequence
C 26	110.2	54.0	7990	6	AX345061	AX345061 Sequence
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C 29	68	33.3	163882	2	AL627325	AL627325 Danio rer
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31	67	32.8	3264	5	AF008592	AF008592 Gallus ga
32	67	32.8	9860	5	AF311289	AF311289 Gallus ga
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36	60.6	29.7	2862	6	AR129834	AR129834 Sequence
37	60.6	29.7	3151	6	AR106402	AR106402 Sequence
38	60.6	29.7	3151	6	AR116704	AR116704 Sequence
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41	59	28.9	2380	9	BC016174	BC016174 Homo sapi
42	59	28.9	2531	9	HUMSCPA	L49431 Homo sapien
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44	59	28.9	2589	6	AR129832	AR129832 Sequence
45	59	28.9	2608	9	HSU45879	U45879 Human inhib

ALIGNMENTS

RESULT 1	AX412124	Sequence 224 from Patent WO0226968.	2100 bp	DNA	linear	PAT 15-JUN-2002
LOCUS	AX412124	Sequence 224 from Patent WO0226968.				
DEFINITION	AX412124					
ACCESSION	AX412124					
VERSION	AX412124.1	GI:21444584				
KEYWORDS						
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
Antisense lap nucleic acids and uses thereof  
Patent: WO 0226968-A 224 04-APR-2002;

University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)

FEATURES  
 LOCUS AR106400  
 DEFINITION Sequence 9 from patent US 6107041  
 ACCESSION AR106400  
 VERSION AR106400.1 GI:12820930  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Mus musculus  
 /db\_xref="taxon:10090"

BASE COUNT 615 a 417 c 482 g 586 t

ORIGIN

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QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGCTAGCTGTTGGAAGACACAGGAGA 180  
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QY 181 ATATCCCCAAATTGCAGATTATC 204  
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REFERENCE  
 AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
 TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
 JOURNAL Patent: US 6107041-A 9 22-AUG-2000;  
 FEATURES Location/Qualifiers  
 source 1..2691  
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 /db\_xref="taxon:10090"

BASE COUNT 819 a 479 c 562 g 831 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 4.5e-61;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120  
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 ACCESSION AR106400  
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 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Mus musculus  
 /db\_xref="taxon:10090"

REFERENCE  
 AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
 TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
 JOURNAL Patent: US 6107041-A 9 22-AUG-2000;  
 FEATURES Location/Qualifiers  
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RESULT 4  
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 DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.  
 ACCESSION U88990  
 VERSION U88990.1 GI:2138318  
 KEYWORDS  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 2691)  
 AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
 TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2691)  
 AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada  
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QY 61 ACATTGGCGGAGCTGGTTCCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120
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QY 121 TGTCTATGGCGCAATAGATAGATGCGAGTGCAGTGTGGAAGACACAGGAGA 180
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Db 927 ATATCCCCAAATTCAGATTATC 950
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MMU36842
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1988)
Uren.A.G., Pakusch.M., Hawkins.C.J., Puls.K.L. and Vaux.D.L.
Cloning and expression of apoptosis inhibitory protein homologs
that function to inhibit apoptosis and/or bind tumor necrosis
factor receptor-associated factors

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JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
MEDLINE 96209843
PUBMED 8643514
REFERENCE 2 (bases 1 to 1988)
AUTHORS Vaux,D.L., Uren,A.G. and Pakusch,M.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall
Institute, Royal Parade, Parkville, Victoria 3050, Australia
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Db 407 TGTCTATGGCGCAATAGATAGATGCGAGTGCAGTGTGGAAGACACAGGAGA 466
QY 181 ATATCCCCAAATTCAGATTATC 204
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**LOCUS** AF304333 2032 bp mRNA linear ROD 19-DEC-2000  
**DEFINITION** Rattus norvegicus clone 1 inhibitor of apoptosis protein 3 mRNA, complete cds.  
**ACCESSION** AF304333  
**VERSION** AF304333.1 GI:11890718  
**SOURCE** Rattus norvegicus.  
**ORGANISM** Rattus norvegicus.  
**REFERENCE** 1 (bases 1 to 2032)  
**AUTHORS** Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.  
**TITLE** Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 2032)  
**AUTHORS** Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verdum St, Nedlands, WA 6907, Australia  
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**DEFINITION** Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA, complete cds.  
**ACCESSION** AF304334  
**VERSION** AF304334.1 GI:11890720  
**SOURCE** Rattus norvegicus.

**ACCESSION** AB033366  
**VERSION** AB033366.1 GI:6045147  
**KEYWORDS** RIAP3.  
**SOURCE** Rattus norvegicus cDNA to mRNA.  
**ORGANISM** Rattus norvegicus  
**REFERENCE** 1 (bases 1 to 2468)  
**AUTHORS** Saito, N.  
**TITLE** Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA  
**JOURNAL** Published Only in DataBase (1999)  
**REFERENCE** 2 (bases 1 to 2468)  
**AUTHORS** Saito, N.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo,  
Department of Neurosurgery; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655,  
Japan [E-mail:nsaito-tyk@umin.ac.jp, Tel:+81-3-5800-8853,  
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**DEFINITION** Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA, complete cds.  
**ACCESSION** AF304334  
**VERSION** AF304334.1 GI:11890720  
**SOURCE** Rattus norvegicus.

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 3032)  
AUTHORS Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and  
Dharmarajan, A.M.  
TITLE Cloning, characterization and regulation of an inhibitor of  
apoptosis protein in the rat corpus luteum  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3032)  
AUTHORS Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2000) Anatomy and Human Biology, University of  
Western Australia, Verdum St, Nedlands, WA 6907, Australia

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DEFINITION AF183429  
ACCESSION AF183429  
VERSION AF183429.1 GI:10765280  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 1491)  
AUTHORS Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.  
TITLE Cloning and characterization of the rat homologues of the Inhibitor  
of Apoptosis protein 1, 2, and 3 genes  
JOURNAL BMC Genomics 3 (1), 5 (2002)  
PUBMED 11860601  
REFERENCE 2 (bases 1 to 1491)  
AUTHORS Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-1999) Department of Biochemistry, Microbiology  
and Immunology, University of Ottawa, 451 Smyth Road, Ottawa,  
Ontario K1H 8M5, Canada

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BASE COUNT 464 a 282 c 357 g 388 t

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Best Local Similarity 95.1%; Pred. No. 2e-55;  
Matches 194; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
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Db 76 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 135  
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QY 61 ACATTGGCGGAGCTGGTTCCTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120  
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Db 136 ACATTGGCGGAGCTGGTTCCTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 195  
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QY 121 TGTCTATCGGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
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Db 196 TGTCTATCGGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 255  
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QY 181 ATATCCCAAAATTCAGATTATC 204  
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Db 256 ATATCCCAAAATTCAGATTATC 279  
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RESULT 10  
E31042  
LOCUS Method for screening substance inhibiting binding to XIAP.  
DEFINITION E31042  
ACCESSION E31042  
VERSION E31042.1 GI:13017307  
KEYWORDS JP 1999326328-A/2.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1659)  
AUTHORS Kunihiro, M.  
TITLE Method for screening substance inhibiting binding to XIAP  
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;  
KUNIHIRO MATSUMOTO  
COMMENT OS Unidentified

	/tissue_type="heart" /clone_lib="lambda gt10, Clontech Laboratories, Cat number HL3018a"
CDS	/dev_stage="fetus" B2..1575 /codon_start=1 /product="IAP-like protein ILP" /protein_id="AAC50518.1" /db_xref="GI:1016688" translation="MTFNSFEKSTCPADINKEEVEEFNRLLTKTANFPSPGSAVSTA TLRAGLTYTGEGDTVRCSFHAAVDWMOYDGSAGRHKKVPNCRFINGFLVLSA TQTSNGLSQNGQQKYVENYLGRDFALDRPSETHDLITLTGGVVDSLIDIIYPDNAM YSSEARLKSFQNWDPIAHILTRELASGLYYTIGDVQCFCCKUKNWPCPDPRMAY EHRHFFPNCFVLGNRLINRSDEAVSDRNFNASTNLPRNPSSADYEAFITFGTWI YSVNKEOLARAGFYALBGDKVKCFHGCGGLTDWKPSDEDWEQHAKWPCKCVLLLEKI GOEYINNHLTHSLIECLVRTTEKTPSILTRIDDIFONPMVOAIRMGFSFDIKKI MEEKIQJSGSNVKSILEVLADVLAQNDMSMEDDSOTLSLOKEISTEQLRRLQEKLK KICMDRNAIVFVPCGHLYTCQAFAVDCPKMCITVTTFKQKIFS"
	misc_feature 163..363 /note="IAP repeat" misc_feature 574..774 /note="IAP repeat" misc_feature 877..1068 /note="IAP repeat" misc_feature 1420..1542 /note="RING finger"
	BASE COUNT    519 A    296 C    385 G    459 T
ORIGIN	
	Query Match         84.3%; Score 172; DB 9; Length 1659; Best Local Similarity   90.2%; Pred. No. 1e-49; Matches 184; Conservative   0; Mismatches 20; Indels   0; Gaps   0;
QY	1 GAGTTTAATAGATTAAAACATTGTCTACTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60       Db
DB	157 GAGTTTAATAGATTAAAACATTGTCTACTCCCAAGTAGTAGTCCTGTTTCAGCATCA 216 
QY	61 ACATTCGCCGCAGCTGGGTTTTCTTTATACCGETGAAGGACACACCGTGCATGTTTCAGT 120     Db
DB	217 ACTATGCCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTTTGTAGT 276 
QY	121 TGTCATGCCGCANTAGATAGATGGCAGTATGGAGACTAGCTGTTTGGAGACACAGGAGA 180 
DB	277 TGTCATGCCGCANTAGATAGATGGCAGTATGGAGACTAGCTGTTTGGAGACACAGGAGA 336 
QY	181 ATATCCCCAAATGCGAGATTTATC 204 
DB	337 GTATCCCCAAATGCGAGATTTATC 360 
RESULT 12	
BC032729	
LOCUS	BC032729                  2086 bp   mRNA   linear   PRI 27-JUN-2002
DEFINITION	Homo sapiens, baculoviral IAP-repeat-containing 4, clone MGC:45369
IMAGE:	5532247, mRNA, complete cds.
ACCESSION	BC032729
VERSION	BC032729.1   GI:21619763
KEYWORDS	MGC,
SOURCE	human. ORGANISM
	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 2086)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabbs-re@mail.nih.gov Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc.mc@nih.gov  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.B., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
 Youngson, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Zoung, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 69 Row: 1 Column: 18  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4502142.

# FEATURES

Location/Qualifiers  
 1..2086  
 /organism="Homo sapiens"  
 /db\_xref="LocusID:331"  
 /db\_xref="taxon:9606"  
 /clone="MGC:45369 IMAGE:5532247"  
 /tissue\_type="Uterus, leiomyosarcoma"  
 /clone\_lib="NIH\_MGC\_71"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
 79..1572  
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 /protein\_id="AAH32729.1"  
 /db\_xref="GI:21619764"  
 /translation="MTFNSFEGSKTCVPADINKEEFVEEFNRLKTFANPPSGPVSA  
 STIARAGFLYTGSDVRCFSCSAANDRWQYGSVAQRHKKVSPNCFEINGVLENSA  
 TQTSNGIQNGQTKVENYLGSRDHFALDRPETHADYLLTGQVVDISDTIYRNPAM  
 YSEARLKSPFNQPDYVAHLTPRELASAGLYITGIGQVQCFCCGGLKLNWPCDRAWS  
 EHRHFPNCFVFLGRNLNIRSDVSSDRNFPNINLPNPMADYEAARIFFTGTWI  
 YSVNQLARAGYALCEGKVKCFHCGGLTDWKPSEDEWQHAQWPGCKVILEOK  
 GOEYINNIHLTHSLECLVTRTEKTPSLTRIDDTIFONPMVOEAIWMGFSFKDIIKI  
 MEKIIQISGNYKSLVIVADLVNAOKDSODSOTSLQKELSTEBQLRLQEEKLC  
 KICMDNRNIIVFVPCGHLVTCQCAENAVDKPCMCYVITFQKIFMS"  
 689 a 341 c 450 g 606 t

## CDS

Query Match 84.3%; Score 172; DB 9; Length 2086;  
 Best Local Similarity 90.2%; Pred. No. 1e-49;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 Qy 1 GAGTTTAATAGATTAAACAACTTGTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 60  
 Db 154 GAGTTTAATAGATTAAACAACTTGTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 213  
 Qy 61 ACATTGGCGGAGCTGGTCTTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 120  
 Db 214 ACATTGGCGGAGCTGGTCTTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 273  
 Qy 121 TGTCTATCGGCAATAGATAGATGCGAGTATGAGACTGAGTGTGGAGACACAGGAGA 180  
 Db 274 TGTCTATCGAGCTAGATAGATGCGCAATATGAGACTGAGTGTGGAGACACAGGAGA 333  
 Qy 181 ATATCCCCAAATTCGAGATTTATC 204  
 Db 334 GTATCCCCAAATTCGAGATTTATC 357

RESULT 13  
 AX429575  
 LOCUS 2404 bp DNA  
 DEFINITION Sequence 38 from Patent. WO0226820.

ACCESSION AX429575  
 VERSION AX429575.1 GI:21540833  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM human.  
 REFERENCE 1 Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,  
 Reinhardt, M.W. and Zeman, S.  
 TITLE Transgenic drosophila melanogaster expressing beta amyloid  
 JOURNAL Patent: WO 0226820-A 38 04-APR-2002;  
 NOVARTIS REFINO VERWALT GMBH (AT)  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 759 a 372 c 525 g 748 t  
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Query Match 84.3%; Score 172; DB 6; Length 2404;  
 Best Local Similarity 90.2%; Pred. No. 1.1e-49;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 Qy 1 GAGTTTAATAGATTAAACAACTTGTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 60  
 Db 109 GAGTTTAATAGATTAAACAACTTGTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 168  
 Qy 61 ACATTGGCGGAGCTGGTCTTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 120  
 Db 169 ACATTGGCGGAGCTGGTCTTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 228  
 Qy 121 TGTCTATCGGCAATAGATAGATGCGAGTATGAGACTGAGTGTGGAGACACAGGAGA 180  
 Db 229 TGTCTATCGAGCTAGATAGATGCGCAATATGAGACTGAGTGTGGAGACACAGGAGA 288  
 Qy 181 ATATCCCCAAATTCGAGATTTATC 204  
 Db 289 GTATCCCCAAATTCGAGATTTATC 312

RESULT 14  
 AX429575  
 LOCUS 2540 bp DNA  
 DEFINITION Sequence 1 from patent US 6087173.  
 ACCESSION AR103281  
 VERSION AR103281.1 GI:12814869  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 2540)  
 AUTHORS Bennett, C.Frank., Ackermann, E.J. and Cowsert, L.M.  
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression  
 JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
 FEATURES Location/Qualifiers  
 source 1..2540  
 /organism="unknown"  
 BASE COUNT 781 a 415 c 571 g 773 t  
 ORIGIN

Query Match 84.3%; Score 172; DB 6; Length 2540;  
 Best Local Similarity 90.2%; Pred. No. 1.1e-49;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
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 Db 109 GAGTTTAATAGATTAAACAACTTGTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 168  
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 Db 169 ACATTGGCGGAGCTGGTCTTCTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 228

QY 121 TGTCTGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGGAGACACAGGAGA 180  
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Db 229 TGTCTGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGGAGACACAGGAAA 288  
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Db 289 GTATCCCCAAATTCAGATTATC 312  
RESULT 15  
AX412118  
LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 218 from Patent WO226968.  
ACCESSION AX412118  
VERSION AX412118.1 GI:21444581  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
TITLE Antisense iap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 218 04-APR-2002;  
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)  
FEATURES  
source  
1. .2540  
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/db\_xref="taxon:9606"  
BASE COUNT 781 a 415 c 570 g 773 t 1 others  
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Query Match 84.3%; Score 172; DB 6; Length 2540;  
Best Local Similarity 90.2%; Pred. No. 1.le-49;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAAACACATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
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QY 61 ACATTTGGCGGAGCTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120  
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QY 121 TGTCTGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGGAGACACAGGAGA 180  
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Db 229 TGTCTGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGGAGACACAGGAAA 288  
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Db 289 GTATCCCCAAATTCAGATTATC 312

Search completed: April 15, 2003, 23:25:25  
Job time: 1035.86 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 136.354 Seconds  
(without alignments)  
3369,223 Million cell updates/sec

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Perfect score: 204  
Sequence: 1 gagttaataagattaaac.....ccccaaattgcagattatc 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	18	Mouse apoptosis in
2	204	100.0	2100	24	Mouse cDNA encoding
3	204	100.0	2691	19	Murine XIAP coding
4	202.4	99.2	1988	18	Mouse inhibitor of
5	172	84.3	1659	21	Human XIAP coding
6	172	84.3	2404	24	DNA of APP related
7	172	84.3	2540	18	Human apoptosis in
8	172	84.3	2540	21	Human X-linked inh
9	172	84.3	2540	24	Human cDNA encoding

10	172	84.3	3000	24	ABK93875
11	172	84.3	5232	19	AAV55038
12	127.8	62.6	7990	24	ABL54307
13	127.8	62.6	7990	24	ABL54308
14	110.2	54.0	7990	24	ABL54308
15	110.2	54.0	7990	24	ABL32159
16	60.6	29.7	2416	18	AAV70841
17	60.6	29.7	2416	24	ABK93874
18	60.6	29.7	2862	18	AAV61592
19	60.6	29.7	3151	19	AAV55043
20	59	28.9	649	24	ABQ60576
21	59	28.9	2580	18	AAV70838
22	59	28.9	2580	24	ABK93871
23	59	28.9	2589	18	AAV61590
24	59	28.9	3532	18	AAV72711
25	59	28.9	3532	20	AAZ22143
26	59	28.9	3532	24	ABN96857
27	59	28.9	3732	19	AAV55040
28	57.4	28.1	2291	22	AAQ6025
29	55.8	27.4	2474	18	AAV70840
30	55.8	27.4	2474	24	ABK93873
31	55.8	27.4	2676	19	AAV55042
32	54.4	26.7	2666	18	AAV70837
33	54.4	26.7	2676	24	ABK93870
34	54.4	26.7	3076	18	AAV72712
35	54.4	26.7	3076	20	AAZ41005
36	54.4	26.7	3076	20	AAZ22096
37	54.4	26.7	3076	24	ABL62746
38	54.4	26.7	3076	24	ABL66325
39	54.4	26.7	6669	19	AAV55039
40	54.4	26.7	6669	24	ABK93876
41	54.2	26.6	1559	24	ABK13197
42	54.2	26.6	1758	24	ABK14677
43	54.2	26.6	1758	24	ABK14678
44	54.2	26.6	4993	22	AAQ03581
45	52.8	25.9	794	24	ABL55635

## ALIGNMENTS

## RESULT 1

AAV70839  
ID AAT70839 standard; cDNA: 2100 BP.

XX AAT70839;

XX 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor m-xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
XX M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
XX ischaemia; myocardial infarction; stroke;  
XX reperfusion injury; toxin-induced liver disease; gene therapy;  
XX diagnosis; ds.

XX Mus sp.

XX key Location/Qualifiers

XX CDS 127..1617

XX FT /\*tag= a

XX WO9706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.

XX 04-AUG-1995; 95US-0511485.

XX (UYOT-) UNIV OTTAWA.

Human cDNA encoding  
Human XIAP coding  
Chemically treated  
Human immune syste  
Chemically treated  
Human immune syste  
Mouse apoptosis in  
Mouse cDNA encoding  
Murine c-IAP. Mus  
Murine XIAP-2 codi  
Human colon cancer  
Human apoptosis in  
Human cDNA encoding  
Human c-IAP1. Hom  
Human inhibitor of  
Human cellular inh  
Gene #3355 used to  
Human XIAP-2 codin  
Angiotensin conver  
Mouse apoptosis in  
Mouse cDNA encoding  
Murine XIAP-1 codi  
Human apoptosis in  
Human cDNA encoding  
Human inhibitor of  
Human cellular inh  
Human cellular inh  
Breast cancer rela  
Lung cancer relate  
Human XIAP-1 codin  
Human cDNA encoding  
Human testes speci  
Human inhibitor of  
Human inhibitor of  
Human IAP-like pro  
AmePV baculovirus-

XX PI Baird S, Korneluk RG, Lliston P, Mackenzie AE;  
 XX DR WPI: 1997-154262/14.  
 XX DR P-PSDB: AAW19384.  
 XX  
 PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease  
 XX  
 PS Claim 11; Page 78-79; 219pp; English.  
 XX  
 CC Human XIAP, hiap-1 and hiap-2 genes, and murine XIAP, hiap-1 and  
 CC hiap-2 genes (AA170836-41) respectively code for a new class of  
 CC mammalian proteins (AAW1581-86) that are inhibitors of apoptosis  
 CC (IAP). The murine XIAP gene (for X-linked IAP gene) sequence was  
 CC constructed from 12 overlapping clones isolated from a mouse  
 CC embryo lambda-gt10 cDNA library and from a mouse FIX II genomic  
 CC library using human XIAP cDNA as probe. IAP nucleic acids can be  
 CC used to express IAP polypeptides in cells and animals to inhibit  
 CC apoptosis, and as primers and probes to identify and isolate  
 CC additional IAP genes, as well as in methods for treating diseases  
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).  
 XX  
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;  
 Query Match 100.0%; Score 204; DB 18; Length 2100;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-61;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
 Db 202 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 261  
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGGTGCATGTTTCAGT 120  
 Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGGTGCATGTTTCAGT 321  
 QY 121 TGTCTATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTGGAAGACACAGGAGA 180  
 Db 322 TGTCTATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTGGAAGACACAGGAGA 381  
 QY 181 ATATCCCAAAATTCGAGATTATC 204  
 Db 382 ATATCCCAAAATTCGAGATTATC 405  
 RESULT 2  
 ABK93872  
 ID ABK93872 standard; cdna; 2100 BP.  
 XX AC ABK93872;  
 XX  
 DT 26-AUG-2002 (first entry)  
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.  
 XX  
 KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200226968-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-CA01379.  
 XX  
 PR 28-SEP-2000; 2000US-0672717.

XX PA (UYOT-) UNIV OTTAWA.  
 XX PI (AEGE-) AEGERA THERAPEUTICS INC.  
 XX DR Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX WPI: 2002-479562/51.  
 XX DR P-PSDB: ABG65666.  
 XX  
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX  
 PS Disclosure; Fig 4; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus, and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;  
 Query Match 100.0%; Score 204; DB 24; Length 2100;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-61;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
 Db 202 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 261  
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGGTGCATGTTTCAGT 120  
 Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGGTGCATGTTTCAGT 321  
 QY 121 TGTCTATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTGGAAGACACAGGAGA 180  
 Db 322 TGTCTATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTGGAAGACACAGGAGA 381  
 QY 181 ATATCCCAAAATTCGAGATTATC 204  
 Db 382 ATATCCCAAAATTCGAGATTATC 405  
 RESULT 3  
 AAV55041  
 ID AAV55041 standard; cdna; 2691 BP.  
 XX  
 AC AAV55041;  
 XX  
 DT 13-NOV-1998 (first entry)  
 DE Murine XIAP coding sequence.  
 XX  
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.  
 XX  
 OS Mus sp.  
 XX  
 PF Key Location/Qualifiers

```

FT CDS 672..2162
FT /*tag= a
FT /product= XIAP
XX
XX W09835693-A2.
XX
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-IB00781.
XX
XX 13-FEB-1997; 97US-0800929.
XX (UYOT-} UNIV OTTAWA.
XX
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX
XX WPI: 1998-467164/40.
XX P-PSDB; AAW69297.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX presence of IAP and NAIP, specifically applied to cancers involving
XX p53 mutations
XX
XX Claim 13; Fig 4; 147pp; English.
XX
XX This sequence encodes the mouse XIAP protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver, nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors.
XX
XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;
XX
XX Query Match 100.0%; Score 204; DB 19; Length 2691;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-61;
XX Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
XX |
XX Db 747 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806
XX |
XX QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 120
XX |
XX Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 866
XX |
XX QY 121 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
XX |
XX Db 867 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926
XX |
XX QY 181 ATATCCCAATTCGAGATTATC 204
XX |
XX Db 927 ATATCCCAATTCGAGATTATC 950
XX |
XX
XX RESULT 4
XX AAT72710
XX ID AAT72710 standard; DNA: 1988 BP.
XX AC AAT72710;
XX
XX 16-SEP-1997 (first entry)
XX

```

```

XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
XX degenerative disease; infectious disease; autoimmune disease;
XX cancer; gene therapy; diagnosis; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 212..1702
XX /*tag= a
XX
XX W09723501-A1.
XX
XX 03-JUL-1997..
XX
XX 20-DEC-1996; 96WO-AU00827.
XX
XX 22-DEC-1995; 95AU-0007275.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI: 1997-350966/32.
XX P-PSDB; AAW19745.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX to modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer
XX
XX Claim 24; Page 44-47; 136pp; English.
XX
XX An isolated nucleic acid molecule (AA72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse
XX liver cDNA library on the basis of homology to Orgyia pseudotsuguta
XX polyhedrosis virus IAP BIR and KING finger amino acid motifs.
XX Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
XX to produce polypeptides useful in methods for modulating apoptosis
XX in animal cells, specifically for treatment, by inhibition, of
XX degenerative and infectious disease or, by promotion, of cancer and
XX autoimmune disease, and can be used for gene therapy of these
XX diseases.
XX
XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
XX
XX Query Match 99.2%; Score 202.4; DB 18; Length 1988;
XX Best Local Similarity 99.5%; Pred. No. 8.5e-61;
XX Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
XX |
XX Db 287 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 346
XX |
XX QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 120
XX |
XX Db 347 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 406
XX |
XX QY 121 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
XX |
XX Db 407 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 466
XX |
XX QY 181 ATATCCCAATTCGAGATTATC 204
XX |
XX Db 467 ATATCCCAATTCGAGATTATC 490
XX |
XX
XX RESULT 5
XX AA248862
XX ID AA248862 standard; cDNA: 1659 BP.
XX
XX

```



AC AA248862;  
 XX  
 DT 24-MAR-2000 (first entry)  
 XX  
 DE Human XIAP coding sequence.  
 XX  
 KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;  
 KW transforming growth factor-beta activated kinase 1; monocyte migration;  
 KW TAK1 binding protein 1; extracellular matrix protein production;  
 KW cell growth inhibitor; beta-amyloid protein deposition;  
 KW immunosuppression; Transforming growth factor-beta; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN JP11326328-A.  
 XX  
 PD 26-NOV-1999.  
 XX  
 PF 13-MAY-1998; 98JP-0130378.  
 XX  
 PR 13-MAY-1998; 98JP-0130378.  
 XX  
 PA (MATS/) MATSUMOTO K.  
 XX  
 DR WPI; 2000-078337/07.  
 DR P-PSDB; AAY59451.  
 XX  
 PT Screening a substance which inhibits combination of the X-linked  
 PT inhibitor of apoptosis protein  
 XX  
 PS Disclosure; Page 28-30; 43pp; Japanese.  
 XX  
 CC This sequence encodes the human XIAP protein.  
 CC The invention relates to a method for screening a substance inhibiting  
 CC the formation of a complex between XIAP and TAB1, in which X-linked  
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
 CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be  
 CC tested are contacted with each other and then the presence or formation  
 CC of a complex between XIAP and TAB1 is detected. The substance can be used  
 CC as a drug for extracellular matrix protein production enhancement, cell  
 CC growth inhibition, monocyte migration, physiologically active substance  
 CC induction, immunosuppression, and beta-amyloid protein deposition. A  
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as  
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type  
 CC I and/or type II receptor is useful as a drug.  
 XX  
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
 Query Match 84.3%; Score 172; DB 21; Length 1659;  
 Best Local Similarity 90.2%; Pred. No. 4.1e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
 DB 157 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 216  
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATATGTTTCAGT 120  
 DB 217 ACATGGCGACGACGAGGTTCTTTATACCGGTGAAGGAGATACCGTGCAGTCTTAGT 276  
 QY 121 TGTATCGCGCAATAGATAGATAGATGACATGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
 DB 277 TGTATCGCTAGTATAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 336  
 QY 181 ATATCCCAATGTCAGATTATC 204  
 DB 337 GTATCCCAAAATGTCAGATTATC 360  
 RESULT 6  
 AAK99405  
 ID AAK99405 standard; DNA; 2404 BP.  
 XX

AC AAK99405;  
 XX  
 DT 27-JUN-2002 (first entry)  
 XX  
 DE DNA of APP related human homologue hcp35211.  
 XX  
 KW Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;  
 KW amyloid precursor protein; tissue-specific expression control; human APP;  
 KW APP pathway modulator; gene therapy; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN Key Location/Qualifiers  
 CDS 692..1528  
 FT /\*tag= a  
 FT /product= "Protein of human homologue hcp35211"  
 FT /note= "No start codon"  
 XX  
 PN WO200226820-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 01-OCT-2001; 2001WO-EP11345.  
 XX  
 PR 29-SEP-2000; 2000US-236893P.  
 PR 14-JUN-2001; 2001US-298309P.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;  
 PI Reinhardt MWM, Zusman S;  
 XX  
 DR WPI; 2002-315796/35.  
 DR P-PSDB; AAO20511.  
 XX  
 PT New transgenic fly, containing DNA encoding an Abeta portion of human  
 PT APP, useful for identifying agents which modulate the APP pathway and  
 PT which can be used to treat Alzheimer's disease.  
 XX  
 PS Example 4; Page 111; 129pp; English.  
 XX  
 CC The invention relates to a transgenic fly whose genome comprises DNA  
 CC encoding a polypeptide having the Abeta portion of human amyloid  
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence  
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in  
 CC the specification. The DNA sequence is operably linked to a tissue-  
 CC specific expression control sequence. Expression of the sequence gives  
 CC the fly an altered phenotype. The purpose of the invention is for  
 CC identifying agents that inhibit or promote the expression and/or function  
 CC of genes or encoded polypeptides which modify the APP pathway. The agent  
 CC is a compound, triple helix DNA, antisense oligonucleotide, double  
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
 CC to treat conditions such as Alzheimer's disease. The agent can be used as  
 CC an APP pathway modulator or in gene therapy. This polynucleotide sequence  
 CC represents the DNA of the APP related human homologue hcp35211.  
 XX  
 SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;  
 Query Match 84.3%; Score 172; DB 24; Length 2404;  
 Best Local Similarity 90.2%; Pred. No. 4.8e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
 DB 109 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168  
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATATGTTTCAGT 120  
 DB 169 ACATGGCGACGACGAGGTTCTTTATACCGGTGAAGGAGATACCGTGCAGTCTTAGT 228  
 QY 121 TGTATCGCGCAATAGATAGATGACATGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
 XX



QY 1 GAGTTTAATAGATAAAACAACTTTGCTTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60  
 DB 109 GAGTTTAATAGATAAAACAACTTTGCTTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 168  
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120  
 DB 169 ACATGGCAGCAGGAGGTTCTTTATACCTGTTGAAGGAGATACCGTGCGGTGCTTTAGT 228  
 QY 121 TGTATGGCGCAATAGATAGATGCGCAATGAGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
 DB 229 TGTATGGCGCAATAGATAGATGCGCAATGAGAGACTCAGCTGTTGGAAGACACAGGAGA 288  
 QY 181 ATATCCCAATTCAGATTTATC 204  
 DB 289 GTATCCCAATTCAGATTTATC 312

RESULT 9  
 ABK93869  
 ID ABK93869 standard; cDNA; 2540 BP.  
 XX  
 AC ABK93869;  
 XX  
 DT 26-AUG-2002 (first entry)  
 XX  
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.  
 XX  
 KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226968-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-CA01379.  
 XX  
 PR 28-SEP-2000; 2000US-0672717.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX  
 DR WPI; 2002-479562/51.  
 DR P-PSDB; ABG65663.  
 XX  
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases -  
 XX  
 PS Disclosure; Flg 1; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
 Query Match 84.3%; Score 172; DB 24; Length 2540;  
 Best Local Similarity 90.2%; Pred. No. 4.9e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATAAAACAACTTTGCTTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60  
 DB 109 GAGTTTAATAGATAAAACAACTTTGCTTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 168  
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120  
 DB 169 ACATGGCAGCAGGAGGTTCTTTATACCTGTTGAAGGAGATACCGTGCGGTGCTTTAGT 228  
 QY 121 TGTATGGCGCAATAGATAGATGCGCAATGAGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
 DB 229 TGTATGGCGCAATAGATAGATGCGCAATGAGAGACTCAGCTGTTGGAAGACACAGGAGA 288  
 QY 181 ATATCCCAATTCAGATTTATC 204  
 DB 289 GTATCCCAATTCAGATTTATC 312

RESULT 10  
 ABK93875  
 ID ABK93875 standard; cDNA; 3000 BP.  
 XX  
 AC ABK93875;  
 XX  
 DT 26-AUG-2002 (first entry)  
 XX  
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
 XX  
 KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226968-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-CA01379.  
 XX  
 PR 28-SEP-2000; 2000US-0672717.  
 XX  
 PA (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX  
 DR WPI; 2002-479562/51.  
 XX  
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases -  
 XX  
 PS Example 2; Fig 15; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of

CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.

SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;  
 Query Match 84.3%; Score 172; DB 24; Length 3000;  
 Best Local Similarity 90.2%; Pred. No. 5.3e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTGCTGTTTCAGCATCA 60  
 |||||  
 DB 765 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTGCTGTTTCAGCATCA 824  
 |||||  
 QY 61 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120  
 |||||  
 DB 825 ACATGGCAGCAGCGAGGTTCTTTATACGTTGGTGAAGGAGATACCGTGGGCTTTAGT 884  
 |||||  
 QY 121 TGTCTATGGCAATAGATAGATGCGAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 180  
 |||||  
 DB 885 TGTCTATGGCAATAGATAGATGCGAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 944  
 |||||  
 QY 181 ATATCCCAAAATTCAGATTATC 204  
 |||||  
 DB 945 GTATCCCAAAATTCAGATTATC 968  
 |||||

RESULT 11  
 AAV55038  
 ID AAV55038 standard; cDNA; 5232 BP.

XX AAV55038;  
 AC  
 XX  
 DT 13-NOV-1998 (first entry)  
 XX Human XIAP coding sequence.

XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 34..1527  
 FT CDS /\*tag= a  
 FT /product= XIAP

XX W09835693-A2.  
 XX 20-AUG-1998.  
 XX 13-FEB-1998; 98WO-1B00781.  
 XX 13-FEB-1997; 97US-0800929.  
 XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX WPI; 1998-467164/40.  
 DR P-PSDB; AAW69294.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 XX Claim 13; Fig 1; 147pp; English.  
 XX This sequence encodes the human XIAP protein, which is an inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.

SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

Query Match 84.3%; Score 172; DB 19; Length 5232;  
 Best Local Similarity 90.2%; Pred. No. 6.8e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTGTTTCAGCATCA 60  
 |||||  
 DB 109 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTGTTTCAGCATCA 168  
 |||||  
 QY 61 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120  
 |||||  
 DB 169 ACATGGCAGCAGCGAGGTTCTTTATACGTTGGTGAAGGAGATACCGTGGGCTTTAGT 228  
 |||||  
 QY 121 TGTCTATGGCAATAGATAGATGCGAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 180  
 |||||  
 DB 229 TGTCTATGGCAATAGATAGATGCGAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 288  
 |||||  
 QY 181 ATATCCCAAAATTCAGATTATC 204  
 |||||  
 DB 289 GTATCCCAAAATTCAGATTATC 312  
 |||||

RESULT 12  
 ABL54307  
 ID ABL54307 standard; DNA; 7990 BP.

XX ABL54307;  
 XX  
 DT 29-JUL-2002 (first entry)  
 XX Chemically treated apoptosis gene #4.

KW Apoptosis; HIV; Bloom syndrome; cardiopathy;  
 KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;  
 KW amyotrophic lateral sclerosis; cancer; ds.

XX Unidentified.  
 XX WO200177164-A2.  
 XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-EP03969.  
 XX 06-APR-2000; 2000DE-1019058.  
 XX 07-APR-2000; 2000DE-1019173.  
 XX 30-JUN-2000; 2000DE-1032529.  
 XX 01-SEP-2000; 2000DE-1043826.

PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2002-017444/02.  
 XX Chemically modified sequences of genes associated with apoptosis are  
 PT useful to determine methylation patterns of genomic DNA samples for  
 PT diagnosis of associated diseases such as cancer  
 XX  
 PS Claim 1; Seq ID #7; 24pp; English.  
 XX  
 CC This invention relates to chemically pre-treated DNA of genes  
 CC associated with apoptosis. The nucleic acids are used to allocate  
 CC patients for specific therapy for HIV infection, Bloom syndrome,  
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus  
 CC infection, renal ischaemia, anyotrophic lateral sclerosis, solid tumours  
 CC and cancers. This nucleotide sequence represents a chemically  
 CC treated apoptosis gene. Even SEQ ID numbers are the complementary  
 CC DNA strands to the odd SEQ ID numbers. The sequence data for this  
 CC patent is not represented in the printed specification but is based on  
 CC information supplied by the European patent office.  
 XX  
 SQ Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;  
 Query Match 62.6%; Score 127.8; DB 24; Length 7990;  
 Best Local Similarity 76.8%; Pred. No. 3.1e-34;  
 Matches 156; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATTAAACAAATTCCTTAACCTCCCAAGTAGTACCTGTTTCAGCATCA 60  
 Db 5109 GAGTTTAATAGATTAAACAAATTCCTTAACCTCCCAAGTAGTACCTGTTTCAGCATCA 60  
 QY 61 ACATTGGCGGAGCTGGTTCCTTATACCGTGAAGGAGACACCGTGCAATGTTTCAGT 120  
 Db 5169 ATATTGGTACGAGTAGGGTTTTTTTATATTGTTGAAGGAGATATCGTCGGTGTTTAGT 5228  
 QY 121 TGTCATCGGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
 Db 5229 TGTATGCTAGTGTAGATAGATGCGTAAATATGAGATTTAGTAGTTGGAAGATATAGGAAA 5288  
 QY 181 ATATCCCAAAATTCAGATTAT 203  
 Db 5289 GTATTTTAAATTTAGATTAT 5311  
 RESULT 13  
 ID ABL32158 standard; DNA; 7990 BP.  
 AC ABL32158;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX Human immune system associated gene SEQ ID NO: 131.  
 DE  
 XX Human; Immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; antihaemic; cytostatic; nootropic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200928-A2.  
 XX  
 XX 03-JAN-2002.  
 PD  
 XX 02-JUL-2001; 2001WO-EP07537.  
 PF  
 XX

PR 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2002-130909/17.  
 XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation  
 XX  
 PS Claim 1; SEQ ID NO 131; 32pp + Sequence Listing; German.  
 XX  
 CC The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 XX  
 SQ Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;  
 Query Match 62.6%; Score 127.8; DB 24; Length 7990;  
 Best Local Similarity 76.8%; Pred. No. 3.1e-34;  
 Matches 156; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
 QY 1 GAGTTTAATAGATTAAACAAATTCCTTAACCTCCCAAGTAGTACCTGTTTCAGCATCA 60  
 Db 5109 GAGTTTAATAGATTAAACAAATTCCTTAACCTCCCAAGTAGTACCTGTTTCAGCATCA 60  
 QY 61 ACATTGGCGGAGCTGGTTCCTTATACCGTGAAGGAGACACCGTGCAATGTTTCAGT 120  
 Db 5169 ATATTGGTACGAGTAGGGTTTTTTTATATTGTTGAAGGAGATATCGTCGGTGTTTAGT 5228  
 QY 121 TGTCATCGGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 180  
 Db 5229 TGTATGCTAGTGTAGATAGATGCGTAAATATGAGATTTAGTAGTTGGAAGATATAGGAAA 5288  
 QY 181 ATATCCCAAAATTCAGATTAT 203  
 Db 5289 GTATTTTAAATTTAGATTAT 5311  
 RESULT 14  
 ID ABL54308/c  
 XX ABL54308 standard; DNA; 7990 BP.  
 AC ABL54308;  
 XX  
 XX 29-JUL-2002 (first entry)  
 DT  
 XX Chemically treated apoptosis gene complementary to gene #4.  
 DE  
 XX Apoptosis; HIV; Bloom syndrome; cardiopathy;  
 KW neurodegenerative disorder; Herpes simplex virus;  
 KW anyotrophic lateral sclerosis; cancer; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200177164-A2.  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-EP03969.  
 PF  
 XX 06-APR-2000; 2000DE-1019058.  
 PR 07-APR-2000; 2000DE-1019173.  
 PR 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 PR

XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2002-017444/02.  
 XX DR Chemically modified sequences of genes associated with apoptosis are  
 XX PT useful to determine methylation patterns of genomic DNA samples for  
 XX PT diagnosis of associated diseases such as cancer.  
 XX PS Claim 1; Seq ID #8; 24pp; English.  
 XX CC This invention relates to chemically pre-treated DNA of genes  
 XX CC associated with apoptosis. The nucleic acids are used to allocate  
 XX CC patients for specific therapy for HIV infection, Bloom syndrome,  
 XX CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus  
 XX CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours  
 XX CC and cancers. This nucleotide sequence represents a chemically  
 XX CC treated apoptosis gene. Even SEQ ID numbers are the complementary  
 XX CC DNA strands to the odd SEQ ID numbers. The sequence data for this  
 XX CC patent is not represented in the printed specification but is based on  
 XX CC information supplied by the European patent office.  
 XX SQ Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;  
 Query Match 54.0%; Score 110.2; DB 24; Length 7990;  
 Best Local Similarity 71.4%; Pred. No. 5e-28;  
 Matches 145; Conservative 0; Mismatches 58; Indels 0; Gaps 0;  
 QY 2 AGTTTAATAGATTAAACAACTTCTGCTTCCCAAGTAGTACCTGTTTCAGCATCAA 61  
 Db 2881 AATTATAATTAATAAATCTTTACTAATTTCCAAATATATATCTTATTCACATCAA 2822  
 QY 62 CATGTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTT 121  
 Db 2821 CACTAACACGACAAATTTCTTTATCTAATAAAAAAATACCGTACGATCTTTAAT 2762  
 QY 122 GTCATGGCGCAATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGAA 181  
 Db 2761 ATCATACACTATAATAATAAATCAATATAAACTCAACAATTAAAAACACAAAAA 2702  
 QY 182 TATCCCCAAATTCGAGATTATC 204  
 Db 2701 TATCCCCAAATTCACAAATTTATC 2679  
 RESULT 15  
 ABL32159/C  
 ID ABL32159 standard; DNA; 7990 BP.  
 XX AC ABL32159;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Human immune system associated gene SEQ ID NO: 132.  
 XX KW Human; immune system disease; cytosine methylation; antiasthmatic;  
 XX KW antiarteriosclerotic; anti-nausea; cytosine; cytosine; cytosine;  
 XX KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 XX KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 XX KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;  
 XX KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 XX KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 XX KW gene; ds.  
 XX OS Homo sapiens.  
 XX PN WO200200928-A2.  
 XX PD 03-JAN-2002.  
 XX PF 02-JUL-2001; 2001WO-EP07537.

XX PR 30-JUN-2000; 2000DE-1032529.  
 XX PR 01-SEP-2000; 2000DE-1043826.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2002-130909/17.  
 XX DR Nucleic acid comprising fragment of chemically modified gene, useful  
 XX PT for diagnosis and treatment of diseases associated with abnormal  
 XX PT cytosine methylation.  
 XX PS Claim 1; SEQ ID NO 132; 32pp + Sequence Listing; German.  
 XX CC The present invention provides a number of human immune system associated  
 XX CC genes which are modified by the methylation of cytosines. The sequences  
 XX CC can be used in the diagnosis and treatment of immune system disorders,  
 XX CC including eye diseases such as retinopathy, neovascular glaucoma and  
 XX CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 XX CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 XX CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 XX CC diseases. The present sequence is a gene of the invention.  
 XX SQ Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;  
 Query Match 54.0%; Score 110.2; DB 24; Length 7990;  
 Best Local Similarity 71.4%; Pred. No. 5e-28;  
 Matches 145; Conservative 0; Mismatches 58; Indels 0; Gaps 0;  
 QY 2 AGTTTAATAGATTAAACAACTTCTGCTTCCCAAGTAGTACCTGTTTCAGCATCAA 61  
 Db 2881 AATTATAATTAATAAATCTTTACTAATTTCCAAATATATATCTTATTCACATCAA 2822  
 QY 62 CATGTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTT 121  
 Db 2821 CACTAACACGACAAATTTCTTTATCTAATAAAAAAATACCGTACGATCTTTAAT 2762  
 QY 122 GTCATGGCGCAATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGAA 181  
 Db 2761 ATCATACACTATAATAATAAATCAATATAAACTCAACAATTAAAAACACAAAAA 2702  
 QY 182 TATCCCCAAATTCGAGATTATC 204  
 Db 2701 TATCCCCAAATTCACAAATTTATC 2679

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 Job time : 143.354 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 25.6771 seconds  
(without alignments)  
2436.494 Million cell updates/sec

Title: US-09-654-743-49  
Perfect score: 204  
Sequence: 1 gagtttaagattcaaaac.....ccccaaattgcagatttacc 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	2	US-08-511-485-9 Sequence 9, Appl
2	204	100.0	2691	3	US-09-212-971-9 Sequence 9, Appl
3	204	100.0	2691	3	US-08-800-929A-9 Sequence 9, Appl
4	204	100.0	2691	4	US-09-617-053A-9 Sequence 9, Appl
5	172	84.3	1588	4	US-09-239-867-3 Sequence 3, Appl
6	172	84.3	2540	2	US-08-511-485-3 Sequence 3, Appl
7	172	84.3	2540	3	US-09-392-580-1 Sequence 1, Appl
8	172	84.3	5232	3	US-09-212-971-3 Sequence 3, Appl
9	172	84.3	5232	3	US-08-800-929A-3 Sequence 3, Appl
10	172	84.3	5232	4	US-09-617-053A-3 Sequence 3, Appl
11	60.6	29.7	2862	4	US-08-569-749-13 Sequence 13, Appl
12	60.6	29.7	2862	5	PCT-US96-12860-13 Sequence 13, Appl
13	60.6	29.7	3151	3	US-09-212-971-13 Sequence 13, Appl
14	60.6	29.7	3151	3	US-08-800-929A-13 Sequence 13, Appl
15	60.6	29.7	3151	4	US-09-617-053A-13 Sequence 13, Appl
16	59	28.9	2580	2	US-08-511-485-7 Sequence 7, Appl
17	59	28.9	2589	4	US-08-569-749-1 Sequence 1, Appl
18	59	28.9	2589	5	PCT-US96-12860-1 Sequence 1, Appl
19	59	28.9	3532	2	US-09-205-204-1 Sequence 1, Appl
20	59	28.9	3732	3	US-09-212-971-7 Sequence 7, Appl
21	59	28.9	3732	3	US-08-800-929A-7 Sequence 7, Appl
22	59	28.9	3732	4	US-09-617-053A-7 Sequence 7, Appl
23	55.8	27.4	2676	3	US-09-212-971-11 Sequence 11, Appl
24	55.8	27.4	2676	3	US-08-800-929A-11 Sequence 11, Appl
25	55.8	27.4	2676	4	US-09-617-053A-11 Sequence 11, Appl
26	54.4	26.7	2676	2	US-08-511-485-5 Sequence 5, Appl
27	54.4	26.7	3076	2	US-09-205-144-1 Sequence 1, Appl

28	54.4	26.7	6569	3	US-09-212-971-5 Sequence 5, Appl
29	54.4	26.7	6569	3	US-08-800-929A-5 Sequence 5, Appl
30	54.4	26.7	6569	4	US-09-617-053A-5 Sequence 5, Appl
31	54.2	26.6	1559	4	US-09-239-867-1 Sequence 1, Appl
32	52.8	25.9	2601	4	US-08-569-749-3 Sequence 3, Appl
33	52.8	25.9	2601	5	PCT-US96-12860-3 Sequence 3, Appl
34	47.6	23.3	5502	3	US-08-836-134-1 Sequence 1, Appl
35	47.6	23.3	5502	4	US-09-493-784-1 Sequence 1, Appl
36	42.4	20.8	1435	5	PCT-US95-05922A-1 Sequence 1, Appl
37	29.8	14.6	10079	2	US-08-476-868-20 Sequence 20, Appl
38	28.6	14.0	711	3	US-09-121-979-3 Sequence 3, Appl
39	28.6	14.0	711	4	US-09-332-319-3 Sequence 3, Appl
40	28.6	14.0	2343	4	US-09-484-970B-119 Sequence 119, App
41	28.6	14.0	9520	4	US-08-952-127-11 Sequence 11, Appl
42	28.4	13.9	168575	4	US-09-426-290-1 Sequence 1, Appl
43	28	13.7	529	4	US-09-602-877A-103 Sequence 103, App
44	28	13.7	1481	1	US-08-136-922-1 Sequence 1, Appl
45	28	13.7	2601	1	US-08-121-713D-53 Sequence 53, Appl

ALIGNMENTS

RESULT 1  
US-08-511-485-9  
; Sequence 9, Application US/08511485  
; Patent No. 5919912  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: MacKenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/511,485  
; FILING DATE: 04-AUG-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 07540/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2100 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: DNA (genomic)  
US-08-511-485-9

Query Match 100.0%; Score 204; DB 2; Length 2100;  
Best Local Similarity 100.0%; Pred. No. 2.7e-60;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 202 GAGTTTAATAGATTAATAAACATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 261  
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Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 321  
QY 121 TGTCTATGGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 180  
Db 322 TGTCTATGGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 381  
QY 181 ATATCCCCAAATTCAGATTATC 204  
Db 382 ATATCCCCAAATTCAGATTATC 405

## RESULT 2

US-09-212-971-9  
; Sequence 9, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212.971B  
; CURRENT FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017.354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030.590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800.929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2691  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-212-971-9

Query Match 100.0%; Score 204; DB 3; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 3e-60;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAATAAACATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
Db 747 GAGTTTAATAGATTAATAAACATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806  
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120  
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866  
QY 121 TGTCTATGGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 180  
Db 867 TGTCTATGGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 926  
QY 181 ATATCCCCAAATTCAGATTATC 204  
Db 927 ATATCCCCAAATTCAGATTATC 950

## RESULT 3

US-08-800-929A-9  
; Sequence 9, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800.929A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030.590  
; FILING DATE: 14-NOV-1996  
; APPLICATION NUMBER: 60/017.354  
; FILING DATE: 26-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bleker-Brady, Kristina  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 07891/009001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2691 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-800-929A-9

Query Match 100.0%; Score 204; DB 3; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 3e-60;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 747 GAGTTTAATAGATTAATAAACATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806  
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Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866  
QY 121 TGTCTATGGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 180  
Db 867 TGTCTATGGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 926  
QY 181 ATATCCCCAAATTCAGATTATC 204  
Db 927 ATATCCCCAAATTCAGATTATC 950

RESULT 4  
US-09-617-053A-9  
; Sequence 9, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:



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; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match      100.0%; Score 204; DB 4; Length 2691;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 747 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806
QY 61 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
DB 807 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 866
QY 121 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 867 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926
QY 181 ATATCCCAAAATTCAGATTATC 204
DB 927 ATATCCCAAAATTCAGATTATC 950

RESULT 5
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match      84.3%; Score 172; DB 4; Length 1588;
Best Local Similarity 90.2%; Pred. No. 2.1e-49;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 109 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
QY 61 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
DB 169 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCGGTGCTTTAGT 228
QY 121 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 229 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288
QY 181 ATATCCCAAAATTCAGATTATC 204

Query Match      84.3%; Score 172; DB 2; Length 2540;
Best Local Similarity 90.2%; Pred. No. 2.5e-49;
Matches 184; Conservative 0; Mismatches 20; Indels 4; Gaps 0;

QY 1 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 109 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
QY 61 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
DB 169 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCGGTGCTTTAGT 228
QY 121 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 229 TGTCAATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288
QY 181 ATATCCCAAAATTCAGATTATC 204
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Db 289 GATATCCCAAAATTCAGATTATC 312

## RESULT 7

US-09-392-580-1

; Sequence 1, Application US/09392580

; Patent No. 6087173

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Elizabeth J. Ackermann

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION

; FILE REFERENCE: RFS-0072

; CURRENT APPLICATION NUMBER: US/09/392,580

; CURRENT FILING DATE: 1999-09-09

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 1

; LENGTH: 2540

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (34)..(1527)

US-09-392-580-1

Query Match 84.3%; Score 172; DB 3; Length 2540;

Best Local Similarity 90.2%; Pred. No. 2.5e-49;

Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60

Db 109 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168

QY 61 ACATTGGCCGAGCTGGTTCCTTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 120

Db 169 ACATTGGCCGAGCTGGTTCCTTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 228

QY 121 TGTCATCGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180

Db 229 TGTCATCGCGCTGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCAGATTATC 204

Db 289 GATATCCCAAAATTCAGATTATC 312

## RESULT 8

US-09-212-971-3

; Sequence 3, Application US/09212971B

; Patent No. 6107041

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 07891/009002

; CURRENT APPLICATION NUMBER: US/09/212,971B

; CURRENT FILING DATE: 1998-12-16

; EARLIER APPLICATION NUMBER: 60/017,354

; EARLIER FILING DATE: 1996-04-26

; EARLIER APPLICATION NUMBER: 60/030,590

; EARLIER FILING DATE: 1996-11-14

; EARLIER APPLICATION NUMBER: 08/800,929

; EARLIER FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 5232

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: variation

; LOCATION: (4623)..(4623)

; OTHER INFORMATION: n can be any nucleotide

; FEATURE:

; NAME/KEY: variation

; LOCATION: (4622)..(4622)

; OTHER INFORMATION: n can be any nucleotide

US-09-212-971-3

Query Match 84.3%; Score 172; DB 3; Length 5232;

Best Local Similarity 90.2%; Pred. No. 3.4e-49;

Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60

Db 109 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168

QY 61 ACATTGGCCGAGCTGGTTCCTTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 120

Db 169 ACATTGGCCGAGCTGGTTCCTTTATACCGTGAAGGAGACACCGTGCATGTTTCAGT 228

QY 121 TGTCATCGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180

Db 229 TGTCATCGCGCTGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCAGATTATC 204

Db 289 GATATCCCAAAATTCAGATTATC 312

## RESULT 9

US-08-800-929A-3

; Sequence 3, Application US/08800929A

; Patent No. 6133437

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF

; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Clark & Elbing LLP

; STREET: 176 Federal Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/800,929A

; FILING DATE: 13-FEB-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/030,590

; FILING DATE: 14-NOV-1996

; APPLICATION NUMBER: 60/017,354

; FILING DATE: 26-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bicker-Brady, Kristina

; REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 5232 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

FEATURE:

NAME/KEY: Other

LOCATION: 1...5232

OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

US-08-800-929A-3

Query Match 84.3%; Score 172; DB 3; Length 5232;

Best Local Similarity 90.2%; Pred. No. 3.4e-49;

Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
|||||  
DB 109 GAGTTTAATAGATTAAACACATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 168  
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120  
|||||  
DB 169 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 228  
QY 121 TGTCTATCGGCAGATAGATAGATGCGAGTATGGAGACTCAGCTGTTGAAGACACAGGAGA 180  
|||||  
DB 229 TGTCTATCGGCAGCTAGATAGATGCGCAATGAGACTCAGCTGTTGAAGACACAGGAGA 288  
QY 181 ATATCCCAAAATTCGAGATTATC 204  
|||||  
DB 289 GTATCCCAAAATTCGAGATTATC 312

#### RESULT 10

US-09-617-053A-3

Sequence 3, Application US/09617053A

Patent No. 6300492

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: MacKenzie, Alexander E

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

FILE REFERENCE: 07891/009003

CURRENT APPLICATION NUMBER: US/09/617,053A

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/800,929

PRIOR FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 5232

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: variation

LOCATION: (4623)...(4623)

OTHER INFORMATION: n can be any nucleotide

NAME/KEY: variation

LOCATION: (4622)...(4622)

OTHER INFORMATION: n can be any nucleotide

US-09-617-053A-3

Query Match 84.3%; Score 172; DB 4; Length 5232;  
Best Local Similarity 90.2%; Pred. No. 3.4e-49;  
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
|||||  
DB 109 GAGTTTAATAGATTAAACACATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 168  
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120  
|||||  
DB 169 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 228  
QY 121 TGTCTATCGGCAGATAGATAGATGCGAGTATGGAGACTCAGCTGTTGAAGACACAGGAGA 180  
|||||  
DB 229 TGTCTATCGGCAGCTAGATAGATGCGCAATGAGACTCAGCTGTTGAAGACACAGGAGA 288  
QY 181 ATATCCCAAAATTCGAGATTATC 204  
|||||  
DB 289 GTATCCCAAAATTCGAGATTATC 312

#### RESULT 11

US-08-569-749-13

Sequence 13, Application US/08569749

Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 2862 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

US-08-569-749-13

#### Query Match

Best Local Similarity 29.7%; Score 60.6; DB 4; Length 2862;

Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 60  
|||||  
DB 608 GAACTCTACCGAATGTCTACATATTCAGCTTTTCCCGAGGAGTCTGTTTCAGAGAGG 667  
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120  
|||||  
DB 668 AGTCTGGCTGCTGCTTTTATTATACAGGTGTGAATGACAAAGTCTTCTTCTGTC 727

QY 121 TGTCTATCCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGAGAGA 180  
Db 728 TGTGGCTGATGTGGTAACTGAAACAAAGGGGACAGTCTCTGTGAAAGACACAGAGAG 787  
QY 181 ATATCCCAAAATTCAGATTAT 203  
Db 788 TTCTATCCAGCTGCAGCTTTGT 810

RESULT 12  
PCT-US96-12860-13  
; Sequence 13, Application PC/TUS9612860  
; GENERAL INFORMATION:  
; APPLICANT: TULARIK, INC.  
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOEACH, TEST, ALBERTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/12860  
; FILING DATE: 06 AUG 1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brezner, David J.  
; REGISTRATION NUMBER: 24,774  
; REFERENCE/DOCKET NUMBER: A-62464/DJB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)781-1989  
; TELEFAX: (415)398-3249  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2862 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US96-12860-13

Query Match 29.7%; Score 60.6; DB 5; Length 2862;  
Best Local Similarity 56.2%; Pred. No. 3.3e-11;  
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAAACAAATTGCTAACCTCCCAAGTAGTAGTCTCTGTTCCAGCATCA 60  
Db 608 GAACCTACCGAATGTCTACATATTCAGCTTTTCCCGAGGAGCTTCTCTCTCAGAGAGG 667  
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 120  
Db 668 AGTCTGGCTGCTGGCTTTTATTACAGGTGTGAATGACAAAGTCAAGTCTCTCTGC 727  
QY 121 TGTCTATCCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGAGAGA 180  
Db 728 TGTGGCTGATGTGTGATTAACCTGAAACAAAGGGGACAGTCTCTGTGAAAGACACAGAG 787  
QY 181 ATATCCCAAAATTCAGATTAT 203  
Db 788 TTCTATCCAGCTGCAGCTTTGT 810

RESULT 13  
US-09-212-971-13  
; Sequence 13, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; CURRENT FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 3151  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-212-971-13  
Query Match 29.7%; Score 60.6; DB 3; Length 3151;  
Best Local Similarity 56.2%; Pred. No. 3.5e-11;  
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
QY 1 GAGTTTAATAGATTAAACAAATTGCTAACCTCCCAAGTAGTAGTCTCTGTTCCAGCATCA 60  
Db 914 GAACCTACCGAATGTCTACATATTCAGCTTTTCCCGAGGAGTCTCTCTCAGAGAGG 973  
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 120  
Db 974 AGTCTGGCTGCTGGCTTTTATTACAGGTGTGAATGACAAAGTCAAGTCTCTCTGC 1033  
QY 121 TGTCTATCCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGAGAGA 180  
Db 1034 TGTGGCTGATGTGTGATTAACCTGAAACAAAGGGGACAGTCTCTGTGAAAGACACAGAG 1093  
QY 181 ATATCCCAAAATTCAGATTAT 203  
Db 1094 TTCTATCCAGCTGCAGCTTTGT 1116

RESULT 14  
US-08-800-929A-13  
; Sequence 13, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA

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; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PS-08-800-929A-13
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Search completed: April 16, 2003, 00:58:54  
Job time : 28.6771 secs

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Query Match          29.7%; Score 60.6; DB 3; Length 3151;
Best Local Similarity 56.2%; Pred. No. 3.5e-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY      1  GAGTTTAATACATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTTCAGCATCA 60
DB      914  GAATCTACCAAGATGCTACATATTCACCTTTTCCAGGGGAGTTCCTGCTCAGAGAGG 973

QY      61  ACATTGGCGCGAGCTGGGTTTTCTTTATACCGGTGAAGGACACCGTGCATGTGTTTCAGT 120
DB      974  AGTCTGGCTGCTGCTGGCTTTTATTATACAGGTGTGAATGACAAAGTCAAGTGTCTTCTGC 1033

QY      121  TGTCAATGCGGCAATAGATAGATAGTCAGCATGGAGACTCAGCTGTTGGGAAGACACAGAGAGA 180
DB      1034  TGTGGCTGTGATTGGGATACGTGAACAAAGGGGACAGTCTCTTTTGAAGAAGCACAGACAG 1093

QY      181  ATATCCCCAAAATTGCAGATTTAT 203
DB      1094  TTCTATCCAGCTGCAGCTTTGT 1116

RESULT 15
US-09-17-053A-13
; Sequence 13, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800, 929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 49.0521 seconds  
(without alignments)  
3648.005 Million cell updates/sec

Title: US-09-654-743-49  
Perfect score: 204  
Sequence: 1 gaggtaataagattaaaac.....ccccaaattgcagattatc 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 593429 seqs, 43858390 residues  
Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*  
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2: /cgn2.6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2.6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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9: /cgn2.6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2.6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2.6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2.6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2.6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2.6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	9	US-09-201-936-9
2	204	100.0	2691	10	US-09-974-592-9
3	172	84.3	2404	9	US-09-964-899-38
4	172	84.3	2540	9	US-09-201-936-3
5	172	84.3	5232	10	US-09-974-592-3
6	60.6	29.7	2416	9	US-09-201-936-41
7	60.6	29.7	3151	10	US-09-974-592-13
8	59	28.9	2580	9	US-09-201-936-7
9	59	28.9	3532	10	US-09-880-107-3354
10	59	28.9	3732	10	US-09-974-592-7
11	57.4	28.1	2291	10	US-09-778-927A-21
12	55.8	27.4	2450	9	US-09-201-936-39
13	55.8	27.4	2675	10	US-09-974-592-11
14	54.4	26.7	2676	9	US-09-201-936-5
15	54.4	26.7	3076	9	US-09-954-531-16
16	54.4	26.7	3076	10	US-09-954-456-1635
17	54.4	26.7	6669	10	US-09-974-592-5
18	47.6	23.3	5504	8	US-08-913-322-1
19	47.6	23.3	6124	8	US-08-913-322-21

20	47.6	23.3	6124	10	US-09-967-768A-184
21	47.6	23.3	6133	8	US-08-913-322-2
22	47.6	23.3	6228	8	US-08-913-322-23
23	36.2	17.7	240	9	US-09-796-692-6687
24	34.6	17.0	240	9	US-09-796-692-3493
25	30.4	14.9	726	10	US-09-772-134B-15
26	29.2	14.3	14707	10	US-09-312-762A-3
27	28.2	13.8	557	10	US-09-772-134B-73
28	28.2	13.8	566	10	US-09-772-134B-114
29	28	13.7	2709	10	US-09-774-490-1
30	27.8	13.6	309	10	US-09-815-242-4570
31	27.8	13.6	312	10	US-09-815-242-8148
32	27.8	13.6	312	10	US-09-815-242-8822
33	27.8	13.6	437	10	US-09-960-352-4026
34	27.8	13.6	521	10	US-09-815-242-2460
35	27.8	13.6	4054	9	US-09-955-363-35
36	27.8	13.6	6378	10	US-09-919-497-40
37	27.8	13.6	6412	10	US-09-769-987-1
38	27.8	13.6	6433	10	US-09-070-927A-104
39	27.8	13.6	13868	7	US-08-781-986A-173
40	27.6	13.5	3773	9	US-10-041-859-1
41	27.6	13.5	58985	9	US-09-301-152-3
42	27.6	13.5	176373	9	US-10-095-407-17
43	27.4	13.4	743	10	US-09-910-943-164
44	27.4	13.4	7992	9	US-09-893-519A-140
45	27.4	13.4	8493	9	US-10-071-766-51

ALIGNMENTS

RESULT 1  
US-09-201-936-9  
; Sequence 9, Application US/09201936  
; Publication No. US20020187946A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: MacKenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201,936  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/1B96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 2100  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-201-936-9

Query Match	100.0%	Score	204	DB 9	Length	2100			
Best Local Similarity	100.0%	Pred. No.	1.7e-61						
Matches	204	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	1	GAGTTTAAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA	60						
Db	202	GAGTTTAAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA	261						
Qy	61	ACATTGGCGCGAGTGGGTTTCTTTATACCGGTGAAGGAGACACGGTGCATGTTTCAGT	120						
Db	262	ACATTGGCGCGAGTGGGTTTCTTTATACCGGTGAAGGAGACACGGTGCATGTTTCAGT	321						

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QY 121 TGTCATCGCGCAATAGATAGATGGCAGTACGCTGTTGGAAGACACAGGAGA 180
      |||||||
Db 322 TGTCATCGCGCAATAGATAGATGGCAGTACGCTGTTGGAAGACACAGGAGA 381
      |||||||

QY 181 ATATCCCAAAATTCAGATTATC 204
      |||||||
Db 382 ATATCCCAAAATTCAGATTATC 405
      |||||||

RESULT 2
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9

Query Match 100.0%; Score 204; DB 10; Length 2691;
Best Local Similarity 100.0%; Pred. No. 1.9e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
      |||||||
Db 747 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806
      |||||||

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 120
      |||||||
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 866
      |||||||

QY 121 TGTCATCGCGCAATAGATAGATGGCAGTACGCTGTTGGAAGACACAGGAGA 180
      |||||||
Db 867 TGTCATCGCGCAATAGATAGATGGCAGTACGCTGTTGGAAGACACAGGAGA 926
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QY 181 ATATCCCAAAATTCAGATTATC 204
      |||||||
Db 927 ATATCCCAAAATTCAGATTATC 950
      |||||||

RESULT 3
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
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; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

Query Match 84.3%; Score 172; DB 9; Length 2404;
Best Local Similarity 90.2%; Pred. No. 3.3e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
      |||||||
Db 109 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
      |||||||

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 120
      |||||||
Db 169 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 228
      |||||||

QY 121 TGTCATCGCGCAATAGATAGATGGCAGTACGCTGTTGGAAGACACAGGAGA 180
      |||||||
Db 229 TGTCATCGCGCAATAGATAGATGGCAGTACGCTGTTGGAAGACACAGGAGA 288
      |||||||

QY 181 ATATCCCAAAATTCAGATTATC 204
      |||||||
Db 289 ATATCCCAAAATTCAGATTATC 312
      |||||||

RESULT 4
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020167946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Stephen
; APPLICANT: Baird, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 84.3%; Score 172; DB 9; Length 2540;
Best Local Similarity 90.2%; Pred. No. 3.4e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
      |||||||
Db 109 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
      |||||||

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 120
      |||||||
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Db 169 AACTGGCAGCAGGAGGTTCTTTATACGGTGAAGGAGATACCGTGGCGTGTTCAGT 228
Qy 121 TGTCTGCGGCAATAGATAGATGCGAGTATGGAGCTCAGCTGTGTGAAGACACAGGAGA 180
Db 229 TGTCTGCGAGCTGTAGATAGATGCGCAATATGGAGCTCAGCAGTGTGAAGACACAGGAAA 288
Qy 181 ATATCCCAAAATTCGAGATTATC 204
Db 289 GTATCCCAAAATTCGAGATTATC 312

RESULT 5
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match 84.3%; Score 172; DB 10; Length 5232;
Best Local Similarity 90.2%; Pred. No. 5e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 GAGTTTAAATAGATTAATAAACATTTGCTTAACCTCCCAAGTAGTACCTGCTGTTTCAGCATCA 60
Db 109 GAGTTTAAATAGATTAATAAACATTTGCTTAACCTCCCAAGTAGTACCTGCTGTTTCAGCATCA 168
Qy 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
Db 169 ACATTGGCGGAGGAGGTTCTTTATACCTGCTGAAGGAGATACCGTGCAGTGTTCAGT 228
Qy 121 TGTCTGCGGCAATAGATAGATGCGAGTATGGAGCTCAGCTGTGTGAAGACACAGGAGA 180
Db 229 TGTCTGCGAGCTGTAGATAGATGCGCAATATGGAGCTCAGCAGTGTGAAGACACAGGAAA 288
Qy 181 ATATCCCAAAATTCGAGATTATC 204
Db 289 GTATCCCAAAATTCGAGATTATC 312

RESULT 6
US-09-201-936-41
; Sequence 41, Application US/09201936
; Publication No. US20020187946A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-41

Query Match 29.7%; Score 60.6; DB 9; Length 2416;
Best Local Similarity 56.2%; Pred. No. 5.6e-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Qy 1 GAGTTTAAATAGATTAATAAACATTTGCTTAACCTCCCAAGTAGTACCTGCTGTTTCAGCATCA 60
Db 215 GAACTCTACCGAATGCTCATATATTCAGCTTTTCCAGGGAGTTCTCTGTCTCAGAGAGG 274
Qy 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
Db 275 AGTCTGGCTCGTGGCTTTTATATACAGGTGTGAATGACAAAGTCAAGTGTCTTCTGC 334
Qy 121 TGTCTGCGGCAATAGATAGATGCGAGTATGGAGCTCAGCTGTGTGAAGACACAGGAGA 180
Db 335 TGTGGCTGTGATGTTGGATACTGGAACACAGGGGACAGCTCTGTGAAAAGCACAGACAG 394
Qy 181 ATATCCCAAAATTCGAGATTAT 203
Db 395 TTCTATCCAGCTGCAGCTTTGT 417

RESULT 7
US-09-974-592-13
; Sequence 13, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA
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PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 3732  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-974-592-7

Query Match 28.9%; Score 59; DB 10; Length 3732;

Best Local Similarity 55.7%; Pred. No. 2.6e-10;

Matches 113; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAATCCCAAGTAGTAGTCTGTTTTCAGCATCA 60  
DB 1515 GAACCTACAGATGCTACATATTCACATTTCCCGCGGGGCTGCTCAGAAAGG 1574  
QY 61 ACATTGGCGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120  
DB 1575 AGCTTGCTGCTGGTGGTTTATATACCTGGTGTGAATGACAGAGTCAATGCTTCTGT 1634  
QY 121 TGTATCGGCAATAGATAGATGAGCAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 180  
DB 1635 TGTGGCCTGATGCTGGATAACTGGAACACTAGGAGACAGTCTTATTCAAAAGCATAAACAG 1694  
QY 181 ATATCCCAAAATTCAGATTAT 203  
DB 1695 CTATATCTAGCTAGCTTTAT 1717

## RESULT 11

US-09-778-927A-21  
Sequence 21, Application US/09778927A  
Patent No. US20020068342A1

GENERAL INFORMATION:

APPLICANT: KHOSRAVI, Rami et al.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL  
VARIANTS OF ALTERNATIVE SPLICING

FILE REFERENCE: 2786-0160P

CURRENT APPLICATION NUMBER: US/09/778,927A

PRIOR FILING DATE: 2001-02-08

PRIOR APPLICATION NUMBER: IL 134453

PRIOR FILING DATE: 2000-02-09

PRIOR APPLICATION NUMBER: IL135341

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 21

LENGTH: 2291

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)-(2291)

OTHER INFORMATION: n - a, c, g, t any unknown or other

US-09-778-927A-21

Query Match 28.1%; Score 57.4; DB 10; Length 2291;

Best Local Similarity 55.2%; Pred. No. 7.3e-10;

Matches 112; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAATCCCAAGTAGTAGTCTGTTTTCAGCATCA 60  
DB 1508 GAACCTACAGATGCTACATATTCACATTTCCCGCGGGGCTGCTCAGAAAGG 1567  
QY 61 ACATTGGCGGAGCTGGTTCCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120  
DB 1568 AGCTTGCTGCTGGTGGTTTATATACCTGGTGTGAATGACAGAGTCAATGTTTCTGT 1627  
QY 121 TGTATCGGCAATAGATAGATGAGCAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 180  
DB 1628 TGTGGCCTGATGCTGGATAACTGGAACACTAGGAGACAGTCTTATTCAAAAGCATAAACAG 1687

QY 181 ATATCCCAAAATTCAGATTAT 203  
DB 1688 CTATATCTAGCTAGCTTTAT 1710

## RESULT 12

US-09-201-936-39

Sequence 39, Application US/09201936

Publication No. US20020187946A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

FILE OF INVENTION: PROSES, AND DETECTION METHODS

FILE REFERENCE: 07891/003003

CURRENT APPLICATION NUMBER: US/09/201,936

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: PCT/IB96/01022

EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER FILING DATE: 1995-12-22

EARLIER APPLICATION NUMBER: 08/511,485

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 39

LENGTH: 2450

TYPE: DNA

ORGANISM: Mus musculus

US-09-201-936-39

Query Match

Best Local Similarity 27.4%; Score 55.8; DB 9; Length 2450;

Matches 111; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAATCCCAAGTAGTAGTCTGTTTTCAGCATCA 60  
DB 240 GAGCTGTACCGATTGCTCCACGATTTCAGCTTTCCAGGGGAGTTCCTGTGTCAGAAAGG 299  
QY 61 ACATTGGCGGAGCTGGTTCCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120  
DB 300 AGTCTGGCTGCTGTGGCTTTTACTACACTGCTGCCAATGACAAGGTCAAGTCTTCTGC 359  
QY 121 TGTATCGGCAATAGATAGATGAGCAGTATGGAGACTGAGTGTGGGAAGACACAGGAGA 180  
DB 360 TGTGGCCTGATGCTAGACACTGGAACAAAGGGACAGTCCCATGGAGACACAGAAAG 419  
QY 181 ATATCCCAAAATTCAGATTAT 203  
DB 420 TTGTACCCACAGCTGCAACTTTGT 442

## RESULT 13

US-09-974-592-11

Sequence 11, Application US/09974592

Patent No. US20020120121A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND

FILE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

FILE REFERENCE: 07891/009004

CURRENT APPLICATION NUMBER: US/09/974,592



QY 181 ATATCCCAAAATTGCAGATT 200  
| | | | | | | | | |  
Db 989 TTGTATCCCTAGCTGCAGATT 1008

Search completed: April 16, 2003, 01:03:52  
Job time : 54.0521 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds  
(without alignments)  
3384.833 Million cell updates/sec

Title: US-09-654-743-49  
Perfect score: 204  
Sequence: 1 gaggtaaatagattaaaac.....ccccaaattgcagattttac 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1:  em_estba:*
2:  em_esthum:*
3:  em_estlin:*
4:  em_estmu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_hic:*
9:  gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gssprt:*
22: em_gssfun:*
23: em_gssmam:*
24: em_gssmus:*
25: em_gssother:*
26: em_gsspro:*
27: em_gssrod:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.8	98.4	698	10	BB653654
2	172	84.3	529	9	AL713196
3	172	84.3	1041	13	BM459898
4	161	78.9	852	14	BQ423165
5	108.2	53.0	822	12	BG502660
6	98.6	48.3	575	13	BM489612

7	93.2	45.7	603	9	AL646185
8	90.2	44.2	676	13	BI392530
9	85.2	41.8	593	13	BJ096099
10	85.2	41.8	681	12	BF611032
11	84.2	41.3	530	13	BJ030180
12	78.8	38.6	603	12	BF614726
13	75	36.8	624	14	BQ552033
14	68	33.3	557	13	BI475879
15	68	33.3	562	13	BI706974
16	68	33.3	565	13	BI706975
17	68	33.3	676	12	BF156225
18	66.4	32.5	574	13	BI706911
19	65.8	32.3	746	9	AF160669
20	62.6	30.7	300	9	AU098645
21	60.6	29.7	633	12	BE912864
22	59	28.9	464	14	BM753271
23	59	28.9	837	12	BG743309
24	59	28.9	855	9	AU131149
25	59	28.9	891	12	BE886741
26	58.6	28.7	613	14	BQ391082
27	58.6	28.7	644	14	BQ389388
28	58	28.4	600	13	BM539590
29	58	28.4	823	12	BG572956
30	57.2	28.0	535	14	BQ618784
31	57.2	28.0	594	12	BF158160
32	57.2	28.0	658	13	BM157229
33	56.8	27.8	801	13	BG934097
34	55.8	27.4	569	12	BG082235
35	55.8	27.4	669	10	BB625247
36	54.8	26.9	756	12	BG773530
37	54.4	26.7	590	10	AW500255
38	54.4	26.7	959	13	BM458775
39	54.2	26.6	742	13	BI829221
40	54.2	26.6	884	13	BI104522
41	54.2	26.6	1020	13	BM545444
42	54.2	26.6	1130	13	BM553272
43	54	26.5	230	10	BE164141
44	53.6	26.3	384	9	AL843873
45	52.8	25.9	475	12	BF615511

## ALIGNMENTS

RESULT 1	BB653654	698 bp	mRNA	linear	EST 26-OCT-2001
LOCUS	BB653654	RIKEN full-length enriched, adult male liver tumor Mus			
DEFINITION	musculus cDNA clone C730014L18 5', mRNA sequence.				
ACCESSION	BB653654				
VERSION	BB653654.1	GI:16487482			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 698)				
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Namura,K., Ono,M., Kouda Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216				

AL646185 AL646185  
BI32530 pppln.pk0  
BJ096099 BJ096099  
BF611032 dg96h06.y  
BJ030180 BJ030180  
BF614726 dg96h08.y  
BQ552033 H401JA06-  
BI475879 fp48b06.x  
BI706974 fq13c08.y  
BI706975 fq13c09.y  
BI156225 fq16c12.y  
BI706911 fq12c09.y  
AF160669 D0274649  
AU098645 AU098645  
BE912864 601665326  
BM753271 K-EST0030  
BG743309 602633394  
AU131149 AU131149  
BE886741 601508903  
BQ391082 NISC.mq16  
BQ389388 NISC.mq07  
BM539590 hb11c10.g  
BG572956 602593929  
BQ618784 fdb07912.  
BF158160 f129d04.y  
BM157229 fv45g04.y  
BG934097 SK1-0386  
BG082235 H3074802-  
BB625247 BB625247  
BG773530 602720264  
AW500255 UI-HF-BNO  
BM458775 AGENCOURT  
BI829221 603079537  
BI104522 602892537  
BM545444 AGENCOURT  
BM553272 AGENCOURT  
BE164141 QV2-HF046  
AL843873 AL843873  
BF615511 de08a04.y

Email: genome-res@gsr.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura  
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
 Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
 Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa  
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
 Hayashizaki, Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.  
 e mouse tissues.

## FEATURES

## source

Location/Qualifiers

1..698

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="C730014118"

/clone\_lib="RIKEN full-length enriched, adult male liver  
tumor"

/sex="male"

/tissue\_type="liver tumor"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5']  
GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTTT 3', cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5']  
GAGAGAGAGATTCTCGAGTTAATTAATTAATCCGCCGCC 3'. cDNA  
was cleaved with BamHI and XbaI. Vector: a modified  
pBluescript KS(+) after bulk excision from Lambda FLC I.  
Tissue was provided by William A. Held, Roswell Park  
Cancer Institute, Department of Molecular and Cellular  
Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose  
assistance we gratefully acknowledge."

## BASE COUNT

## ORIGIN

Query Match 98.4%; Score 200.8; DB 10; Length 698;  
 Best Local Similarity 99.0%; Pred. No. 2.9e-57;  
 Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGTTAATAGATTAACAACTTGGCTTAACCTCCAGTAGTAGTCTCTGTTTCAGCATCA 60

Db 451 GAGTTAATAGATTAACAACTTGGCTTAACCTCCAGTAGTAGTCTCTGTTTCAGCATCA 510

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120

Db 511 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 570

QY 121 TGTCTATGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180

Db 571 TGTCTATGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 530

QY 181 ATATCCCAAAATTCAGATTATC 204

Db 631 ATATCCCAAAATTCAGATTATC 654

## RESULT 2

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## MIPS

## Am Klopferspitz 18a D-82152 Martinsried, Germany

## This is the 5' sequence of the clone insert

## Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

## Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

## Sequenced by GBF (National Research Centre for Biotechnology Ltd.,

## Braunschweig/Germany) within the cDNA sequencing consortium of the

## German Genome Project.

## No sl sequence available.

## This clone (DKFZp686M1895) is available at the RZPD in Berlin.

## Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

## Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## Location/Qualifiers

## 1..529

## /organism="Homo sapiens"

## /db\_xref="taxon:9606"

## /clone="DKFZp686M1895"

## /clone\_lib="886 (synonym: hlec3)"

## /tissue\_type="human skeletal muscle"

## /dev\_stage="adult"

## /lab\_host="DH10B"

## /note="Vector: pTriplex2; Site 1: SfiIA; Site 2: SfiIB;

## CDNA-collection"

## BASE COUNT 165 a 96 c 126 g 142 t

## ORIGIN

## Query Match 84.3%; Score 172; DB 9; Length 529;

## Best Local Similarity 90.2%; Pred. No. 1.6e-47;

## Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

## QY 1 GAGTTTATAGATTAAACAACTTGGCTTAACCTCCAGTAGTAGTCTCTGTTTCAGCATCA 60

## Db 137 GAGTTTATAGATTAAACAACTTGGCTTAACCTCCAGTAGTAGTCTCTGTTTCAGCATCA 196

## QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120

## Db 197 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 256

## QY 121 TGTCTATGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180

## Db 257 TGTCTATGCGCTGTAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 316

## QY 181 ATATCCCAAAATTCAGATTATC 204

## Db 317 GTATCCCAAAATTCAGATTATC 340

```

RESULT 3
BM459898      1041 bp  mRNA  linear  EST 05-FEB-2002
LOCUS        AGENCOURT_6422054 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
DEFINITION   5', mRNA sequence.
ACCESSION    BM459898
VERSION      BM459898
KEYWORDS     BM459898.1 GI:18508938
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 1041)
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-r@mail.nih.gov
              Tissue Procurement: ATCC/DCTD/DMP
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM12215 row: d column: 08
              High quality sequence stop: 567.
FEATURES     Location/Qualifiers
              1..1041
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:5532247"
              /clone_lib="NIH_MGC_71"
              /tissue_type="telomerosarcoma"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI;
              Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
              Average insert size 2.1 kb."
              297 a 208 c 266 g 269 t 1 others
BASE COUNT   297 a 208 c 266 g 269 t
ORIGIN
Query Match      84.38; Score 172; DB 13; Length 1041;
Best Local Similarity 90.28; Pred. No. 2.3e-47;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
    |||||
DB 142 GAGTTTAAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 201
    |||||

QY 61 ACATTGGCGGAGGTGGGTTTCTTTATACCGGTGAAGAGACACGTCGCAATGTTTCAGT 120
    |||||
DB 202 ACATTGGCGGAGGTGGGTTTCTTTATACCGGTGAAGAGATACCGTGGCGTCTTAGT 261
    |||||

QY 121 TGTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 180
    |||||
DB 262 TGTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 321
    |||||

QY 181 ATATCCCCAAATTCAGATTTATC 204
    |||||
DB 322 GTATCCCCAAATTCAGATTTATC 345
    |||||

RESULT 4
BQ423165      852 bp  mRNA  linear  EST 23-MAY-2002
LOCUS        AGENCOURT_7761069 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062005
DEFINITION   5', mRNA sequence.
ACCESSION    BQ423165
VERSION      BQ423165
KEYWORDS     BQ423165.1 GI:21118480
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 852)
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-r@mail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: CLONETECH Laboratories, Inc.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 852)
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-r@mail.nih.gov
              Tissue Procurement: ATCC/DCTD/DMP
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13332 row: m column: 14
              High quality sequence stop: 503.
FEATURES     Location/Qualifiers
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              /db_xref="taxon:9606"
              /clone="IMAGE:6062005"
              /clone_lib="NIH_MGC_72"
              /tissue_type="melanotic melanoma"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: skin; Vector: PCMV-SPORT6; Site_1: NotI;
              Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
              Average insert size 2 kb. Library constructed by Life
              Technologies."
              210 a 191 c 242 g 209 t
BASE COUNT   210 a 191 c 242 g 209 t
ORIGIN
Query Match      78.98; Score 161; DB 14; Length 852;
Best Local Similarity 89.88; Pred. No. 1.2e-43;
Matches 184; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 1 GAGTTTAAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
    |||||
DB 398 GAGTTTAAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 457
    |||||

QY 61 ACATTGGCGGAGGTGGGTTTCTTTATACCGGTGAAGAGACACGTCGCAATGTTTCAGT 120
    |||||
DB 458 ACATTGGCGGAGGTGGGTTTCTTTATACCGGTGAAGAGATACCGTGGCGTCTTAGT 517
    |||||

QY 121 TGTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 180
    |||||
DB 518 TGTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 577
    |||||

QY 181 ATAT-CCCCAAATTCAGATTTATC 204
    |||||
DB 578 GTATCCCCAAATTCAGATTTATC 602
    |||||

RESULT 5
BG502660      822 bp  mRNA  linear  EST 27-MAR-2001
LOCUS        602549490P1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
DEFINITION   mRNA sequence.
ACCESSION    BG502660
VERSION      BG502660
KEYWORDS     BG502660.1 GI:13464177
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 822)
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
              Email: cgaabs-r@mail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: CLONETECH Laboratories, Inc.

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source
1. .603
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TCas047014"
/dev_stage="XGC-gastrula"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dr primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into PCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT 165 a 131 c 150 g 156 t 1 others
ORIGIN
Query Match 45.7%; Score 93.2; DB 9; Length 603;
Best Local Similarity 67.5%; Pred. No. 1.2e-20;
Matches 131; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 10 AGATTAAACATTTGCTAACTCCCAAGTAGTAGTCTCTGTTTCAGCATCAACATTGGCG 69
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 163 AGACTGGCGTCTTGTGTAATCTCCCAAGTAGTAGTCTCTGTTTCAGCATCAACATTGGCG 222
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 70 CGAGCTGGGTTCTTTATACGGTGAAGGAGACACCGTCAATCTTCAGTTGTCATGCG 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 223 CGGCCGGCTTCTATTACCTGGAGATGGAGATCGATCGATCAAGTCTTTAGCTGCTGGCT 282
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 130 GCAATAGATAGATGGCAGTATGAGACTCAGCTCTTGGAGACACAGGAGAAATATCCCA 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 283 ATGTTGAAGCGTGGCAGCATGGAGACACGCAATTTGGCAAGCAGCGGAAATATCCCA 342
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 190 AATGCGAGATTAT 203
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 343 AACTGTAATTTAT 356
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
BI392530 676 bp mRNA linear EST 06-AUG-2001
LOCUS
DEFINITION
pgpin.pk008.d6 Normalized Chicken Pituitary/Hypothalamus/Pineal
Library Gallus gallus cDNA clone pgpin.pk008.d6 5' similar to
gb|AAG22969.1|AF183429.1 (AF183429) inhibitor of apoptosis protein
3 [Rattus norvegicus], mRNA sequence.
ACCESSION BI392530
VERSION BI392530.1 GI:15085812
KEYWORDS EST.
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 676)
AUTHORS Porter,T.E. and Cogburn,L.A.
TITLE ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
library USDA/IRAFS Animal Genome Project
JOURNAL Unpublished (2001)
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES
source
1. .676
/organism="Gallus gallus"
/strain="Commercial broiler chicken"
/db_xref="taxon:9031"
/clone="pgpin.pk008.d6"
/clone_lib="Normalized Chicken
Pituitary/Hypothalamus/Pineal Library"
/sex="Male and Female"
/tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (dl2,dl4,dl9); post-hatch (wl,w3,w5)

, w7, w9"
/lab_host="E. Coli EMDH10B"
/note="Vector: PCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue at different
ages. Single pass sequencing from 5'-end"
BASE COUNT 141 a 156 c 194 g 166 t 19 others
ORIGIN
Query Match 44.2%; Score 90.2; DB 13; Length 676;
Best Local Similarity 64.8%; Pred. No. 1.4e-19;
Matches 125; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 11 GATTAAACATTTGCTAACTCCCAAGTAGTAGTCTCTGTTTCAGCATCAACATTGGCG 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 419 GACTAGGAACCTTTGTGGAGTTTCCCATGATTTCCAGTTTCAGCATCGCGTAGCTC 478
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 71 GAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTCAATCTTCAGTTGTCATGCGG 130
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 479 GAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTCAATCTTCAGTTGTCATGCGG 538
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 131 CAATAGATAGATGGCAGTATGAGACTCAGCTCTTGGAGACACAGGAGAAATATCCCA 190
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 539 CTGTTGAAGGATGGAGCGCTNNNGATTCTGCAATTTGACAGACACAAAACCTTNNNCAG 598
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 191 ATTGCAGATTAT 203
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 599 NNNGCAGATTAT 611
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
BJ096099 593 bp mRNA linear EST 12-DEC-2001
LOCUS
DEFINITION
Xenopus laevis cDNA clone XLI52K19 5', mRNA sequence.
ACCESSION BJ096099
VERSION BJ096099.1 GI:17596868
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 593)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
,Y.
EXTRACTED FROM in X. laevis embryo
Unpublished (2001)
CONTACT Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
LOCATION/Qualifiers
1. 593
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XLI52K19"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
library"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; CDNAS
were oligo-dr primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Welcomme/CRC Institute)."
BASE COUNT 175 a 129 c 137 g 152 t
ORIGIN
Query Match 41.8%; Score 85.2; DB 13; Length 593;
Best Local Similarity 64.9%; Pred. No. 6.5e-18;

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Matches 126; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 10 AGATTAACAACTTCTTACTTCCCAAGTAGTAGTCTGTTTCAGCATCAACATGGCG 69
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Db 54 AGACTGGCCCTCTTCTTAAATTTCAAGTAGTACCTCTGTTTCTGCCCCAGCAGTAGCA 113
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QY 70 CGAGCTGGGTTCTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTTGTCATGGC 129
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Db 114 CGGCGGGCTTTTATTACACTGGAGATGGAGACCGAGTAAGTGTTTTACGTGTATGGCT 173
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QY 130 GCAATAGATAGATGGAGACTGAGACTGAGTGGGAAGACAGGAGATATCCCA 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 ATGGTCGAAGATGGAGCATGGAGACACCGCAATCGGCAAGCATCGGAAATATCTCCA 233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 AATTGCAGATTAT 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 AACTGTAATTCAT 247
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RESULT 10
BF611032 681 bp mRNA linear EST 14-DEC-2000
LOCUS d396h06.y1 Wellcome CRC PRN3 oocyte Xenopus laevis cDNA clone
DEFINITION IMAGE:3436642 5' similar to SW:1AP3_MOUSE Q60989 INHIBITOR OF
APOPTOSIS PROTEIN 3 ; mRNA sequence.
ACCESSION BF611032
VERSION BF611032
KEYWORDS EST.
SOURCE BF611032.1 GI:11780268
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 681)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washu Xenopus EST project, 1999
Unpublished (1999)
Other ESTs: dd96h06.x1
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40bp from Gibco
High quality sequence stop: 513.
FEATURES
source
    Location/Qualifiers
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            /db_xref="taxon:8355"
            /clone="IMAGE:3436642"
            /clone_lib="Wellcome CRC PRN3 oocyte"
            /tissue_type="oocyte"
            /lab_host="DH10B (phage-resistant)"
            /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
            were oligo-dT primed and directionally cloned. Staging
            according to Nieuwkoop and Faber. Library was constructed
            by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon
            (Wellcome/CRC Institute)."
BASE COUNT 198 a 149 c 155 g 177 t 2 others
Query Match 41.8%; Score 85.2; DB 12; Length 681;
Best Local Similarity 64.9%; Pred. No. 7e-18;

Matches 126; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 10 AGATTAACAACTTCTTACTTCCCAAGTAGTAGTCTGTTTCAGCATCAACATGGCG 69
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Db 54 AGACTGGCCCTCTTCTTAAATTTCAAGTAGTACCTCTGTTTCTGCCCCAGCAGTAGCA 216
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QY 70 CGAGCTGGGTTCTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTTGTCATGGC 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 CGGCGGGCTTTTATTACACTGGAGATGGAGACCGAGTAAGTGTTTTACGTGTATGGCT 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 130 GCAATAGATAGATGGAGACTGAGACTGAGTGGGAAGACAGGAGATATCCCA 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 ATGGTCGAAGATGGAGCATGGAGACACCGCAATCGGCAAGCATCGGAAATATCTCCA 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 AATTGCAGATTAT 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 AACTGTAATTCAT 350
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RESULT 11
BJ030180 530 bp mRNA linear EST 05-DEC-2001
LOCUS BJ030180 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL003f24 5', mRNA sequence.
ACCESSION BJ030180
VERSION BJ030180
KEYWORDS EST.
SOURCE BJ030180.1 GI:17371606
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 530)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
    Location/Qualifiers
        1..530
            /organism="Xenopus laevis"
            /db_xref="taxon:8355"
            /clone="XL003f24"
            /clone_lib="NIBB Mochii normalized xenopus neurula
            library"
            /tissue_type="whole embryo"
            /dev_stage="stage 15"
            /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
            were oligo-dT primed and directionally cloned. Staging
            according to Nieuwkoop and Faber. Library is subtracted
            and was constructed by N. Garrett and A.M. Zorn,
            (Wellcome/CRC Institute)."
BASE COUNT 156 a 112 c 125 g 136 t 1 others
Query Match 41.3%; Score 84.2; DB 13; Length 530;
Best Local Similarity 64.4%; Pred. No. 1.3e-17;
Matches 125; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 10 AGATTAACAACTTGTCACTTCCCAAGTAGTAGTCTGTTTCAGCATCAACATGGCG 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 AGACTGGCCCTCTTCTTAAATTTCAAGTAGTAGTCTGTTTCTGCCCCAGCAGTAGCA 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 CGAGCTGGGTTCTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTTGTCATGGC 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 186 CGGCGGGCTTTTATTACACTGGAGATGGAGACCGAGTAAGTGTATAGCTGTATGCT 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db  
550 GAGTTTAATAGATTAAACAATTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 609



QY 129 GGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAAGACACAGGAGGATATCCCC 188  
Db 157 GACTGCTGACAACTGGCAGTCTGTGACTGTCCCGCAGAGCGCCACAAACAGCTATCCCC 216  
QY 189 AAATTGCAGATTTATC 204  
Db 217 CACTGCAGCTTCATC 232

Search completed: April 16, 2003, 00:55:03  
Job time : 1978.083 secs

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 Seconds  
(without alignments)  
5753.635 Million cell updates/sec

Title: US-09-654-743-50  
Perfect score: 204  
Sequence: 1 gaagaaagcagattgaagtc.....ttcccaattgctttttgtt 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

GenEmbl:\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
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31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htg\_mus.\*  
34: em.htg\_pln.\*  
35: em.htg\_rod.\*  
36: em.htg\_man.\*  
37: em.htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	204	100.0	2100	6	AX412124	Sequence
2	204	100.0	2691	6	AR106400	Sequence
3	204	100.0	2691	6	AR116702	Sequence
4	204	100.0	2691	10	MM088990	U88990 Mus musculus
5	202.4	99.2	1988	10	MMU36842	U36842 Mus musculus
6	178.4	87.5	2032	10	AF304333	AF304333 Rattus no
7	178.4	87.5	2468	10	AB033366	AB033366 Rattus no
8	178.4	87.5	3032	10	AF304334	AF304334 Rattus no
9	176.8	86.7	1491	10	AF183429	AF183429 Rattus no
10	172	84.3	1659	6	E31042	E31042 Method for
11	172	84.3	1659	9	HSU32974	U32974 Human IAP-1
12	172	84.3	2086	9	BC032729	BC032729 Homo sapi
13	172	84.3	2540	6	AR103281	AR103281 Sequence
14	172	84.3	2540	6	AX412118	AX412118 Sequence
15	172	84.3	2540	9	HSU45880	U45880 Human X-lin
16	172	84.3	3000	6	AX412131	AX412131 Sequence
17	172	84.3	5232	6	AR106397	AR106397 Sequence
18	172	84.3	5232	6	AR116699	AR116699 Sequence
19	172	84.3	133391	9	HSU311561	AL121601 Human DNA
20	172	84.3	201197	2	HS424312	282207 Homo sapien
21	161	78.9	2404	6	AX429575	AX429575 Sequence
22	156	76.5	1758	6	AX370787	AX370787 Sequence
23	154.4	75.7	1758	6	AX370789	AX370789 Sequence
24	154.4	75.7	2032	9	AF420440	AF420440 Homo sapi
25	154.4	75.7	4993	6	AX104968	AX104968 Sequence
26	154.4	75.7	4993	9	AF164682	AF164682 Homo sapi
27	154.4	75.7	144301	9	AC010467	AC010467 Homo sapi
28	154.4	75.7	165662	9	AC092070	AC092070 Homo sapi
29	135.8	66.6	1740	5	AF451854	AF451854 Gallus ga
30	121.8	59.7	184439	2	AP003085	AP003085 Homo sapi
31	121.8	59.7	187568	9	AP002967	AP002967 Homo sapi
32	120.8	59.2	7990	6	AX281265	AX281265 Sequence
33	120.8	59.2	7990	6	AX345060	AX345060 Sequence
34	103.8	50.9	7990	6	AX281266	AX281266 Sequence
35	103.8	50.9	7990	6	AX345061	AX345061 Sequence
36	81.4	39.9	2563	9	HUMSCP8	L49432 Homo sapien
37	81.4	39.9	2601	6	AR129833	AR129833 Sequence
38	81.4	39.9	2676	6	AX412120	AX412120 Sequence
39	81.4	39.9	2916	9	HSU45878	U45878 Human inhib
40	81.4	39.9	3076	6	AR076287	AR076287 Sequence
41	81.4	39.9	3076	6	AX330574	AX330574 Sequence
42	81.4	39.9	3076	6	AX334153	AX334153 Sequence
43	81.4	39.9	3076	9	HSU37546	U37546 Human IAP h
44	81.4	39.9	3734	6	AX055871	AX055871 Sequence
45	81.4	39.9	3734	6	AX472621	AX472621 Sequence

## ALIGNMENTS

RESULT 1	AX412124	Sequence 224 from Patent WO0226968.	2100 bp	DNA	linear	PAT 15-JUN-2002
LOCUS	AX412124	Sequence 224 from Patent WO0226968.				
DEFINITION	AX412124					
ACCESSION	AX412124					
VERSION	AX412124.1	GI:21444584				
KEYWORDS						
SOURCE	house mouse.					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE						
AUTHORS	Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.					
TITLE	Antisense iap nucleic acids and uses thereof					
JOURNAL	Patent: WO 0226968-A 224 04-APR-2002;					

University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)  
source  
Location/Qualifiers  
1. .2100  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
BASE COUNT 615 a 417 c 482 g 586 t  
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2100;  
Best Local Similarity 100.0%; Pred. No. 4.6e-52;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60  
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Db 613 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 672  
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QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120  
|||||  
Db 673 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 732  
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QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180  
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Db 733 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 792  
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QY 181 CACTTTCCCAATGCTTTTGT 204  
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Db 793 CACTTTCCCAATGCTTTTGT 816  
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RESULT 2  
AR106400  
LOCUS  
DEFINITION  
Sequence 9 from patent US 6107041.  
ACCESSION  
AR106400  
VERSION  
AR106400.1 GI:12820930  
KEYWORDS  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 2691)  
AUTHORS  
Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE  
Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL  
Patent: US 6107041-A 9 22-AUG-2000;  
FEATURES  
Location/Qualifiers  
source  
1. .2691  
/organism="unknown"  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 4.5e-52;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60  
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QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120  
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Db 1218 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 1277  
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QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180  
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Db 1278 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 1337  
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QY 181 CACTTTCCCAATGCTTTTGT 204  
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Db 1338 CACTTTCCCAATGCTTTTGT 1361  
|||||

RESULT 3  
AR106400  
LOCUS  
DEFINITION  
Sequence 9 from patent US 6107041.  
ACCESSION  
AR106400  
VERSION  
AR106400.1 GI:12820930  
KEYWORDS  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 2691)  
AUTHORS  
Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE  
Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL  
Patent: US 6107041-A 9 22-AUG-2000;  
FEATURES  
Location/Qualifiers  
source  
1. .2691  
/organism="unknown"  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 4.5e-52;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60  
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Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 1217  
|||||

QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120  
|||||  
Db 1218 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 1277  
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QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180  
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Db 1278 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 1337  
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QY 181 CACTTTCCCAATGCTTTTGT 204  
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Db 1338 CACTTTCCCAATGCTTTTGT 1361  
|||||

AR116702  
LOCUS  
DEFINITION  
Sequence 9 from patent US 6133437.  
ACCESSION  
AR116702  
VERSION  
AR116702.1 GI:14097024  
KEYWORDS  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 2691)  
AUTHORS  
Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE  
Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL  
Patent: US 6133437-A 9 17-OCT-2000;  
FEATURES  
Location/Qualifiers  
source  
1. .2691  
/organism="unknown"  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 4.5e-52;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60  
|||||  
Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 1217  
|||||

QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120  
|||||  
Db 1218 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 1277  
|||||

QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180  
|||||  
Db 1278 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 1337  
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QY 181 CACTTTCCCAATGCTTTTGT 204  
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Db 1338 CACTTTCCCAATGCTTTTGT 1361  
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RESULT 4  
MMU88990  
LOCUS  
DEFINITION  
Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.  
ACCESSION  
U88990  
VERSION  
U88990.1 GI:2138318  
KEYWORDS  
SOURCE  
Mus musculus.  
ORGANISM  
Mus musculus.  
REFERENCE  
1 (bases 1 to 2691)  
AUTHORS  
Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
TITLE  
Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 2691)  
AUTHORS  
Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada  
FEATURES  
Location/Qualifiers  
source  
1. .2691  
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1. .2691  
/gene="miap-3"  
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/ gene="miap-3"
/ number=1
672..2162
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/ note="MIAP-3"
/ codon_start=1
/ product="X-linked inhibitor of apoptosis"
/ protein_id="AA858376.1"
/ db_xref="GI:2138319"
/ translation="MTFNSFEGTRTFVLADNKKDEEFVEENRLKTPANFPSSPVSA
AQLARAGFLYTGEGTVQCFCHAAIDRWQYGSAGVHRRIISPNCRFINGFYFENGA
AQTNPQIQNGQKSENCVGNRNPFPADRPETHADYLLRTGOVVDISDTIYPNPAM
CSEARLKSPONPDYAHLPRELASGLYTGADDOVQCFCCGKLNWPCDRAMS
EHRHFPCFVLGRNVNVRSEGVSSDRNPSTNSPRNPAMAEYARIVTGTWTS
SVNKEQLARAGFYALGEGDKVCKFCHCGGLTDWKPSEDPPWQHAKWYPCCKYLLDEKG
QEIYNNIHLTHSLESLGRTAEKTPSLTKKIDDTIFQNPVQEAIRMGFSFADLKKT
EERKIQSGSYLSLEVLIALDLVSAQKNTDESSQTSLOKDISITEEQRLQEEKLK
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819 a 479 c 562 g 831 t

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Best Local Similarity 100.0%; Pred. No. 4.5e-52;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1218 GAGTTAGCTAGTGGCTCTACTACACAGGGCTGTATGATCAAGTGCATGCTTTTGT 1277
Qy 121 TGTGGGGAAACTGAAAAATGGAAACCTGTGATCGTGGCTGTACAGACACAGGAGA 180
Db 1278 TGTGGGGAAACTGAAAAATGGAAACCTGTGATCGTGGCTGTACAGACACAGGAGA 1337
Qy 181 CACTTTCCCAATTGCTTTTGT 204
Db 1338 CACTTTCCCAATTGCTTTTGT 1361

RESULT 5
LOCUS MMU36842 1986 bp mRNA linear ROD 05-JUN-1996
DEFINITION Mus musculus IAP homolog A (MIHA) mRNA, complete cds.
ACCESSION U36842
VERSION U36842.1 GI:1145260
KEYWORDS house mouse strain=C57 Black 6 x CBA.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1988)
Uren,A.G., Pakusch,M., Hawkins,C.J., Puls,K.L. and Vaux,D.L.
Cloning and expression of apoptosis inhibitory protein homologs
that function to inhibit apoptosis and/or bind tumor necrosis
factor receptor-associated factors

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
MEDLINE 96209843
PUBMED 8643514
REFERENCE 2 (bases 1 to 1988)
AUTHORS Vaux,D.L., Uren,A.G. and Pakusch,M.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall
Institute, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES
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1..1988
/organism="Mus musculus"
/strain="C57 Black 6 x CBA"
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CSEARLKSPONPDYAHLPRELASGLYTGADDOVQCFCCGKLNWPCDRAMS
EHRHFPCFVLGRNVNVRSEGVSSDRNPSTNSPRNPAMAEYARIVTGTWTS
SVNKEQLARAGFYALGEGDKVCKFCHCGGLTDWKPSEDPPWQHAKWYPCCKYLLDEKG
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/ note="BIR repeat 2"
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605 a 367 c 459 g 557 t

BASE COUNT
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 1.4e-51;
Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTAGCTATTCATTACCCCCAGA 60
Db 698 GAAGAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTAGCTATTCATTACCCCCAGA 757
Qy 61 GAGTTAGCTAGTGGCTCTACTACACAGGGCTGTATGATCAAGTGCATGCTTTTGT 120
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Db 818 TGTGGGGAAACTGAAAAATGGAAACCTGTGATCGTGGCTGTACAGACACAGGAGA 877
Qy 181 CACTTTCCCAATTGCTTTTGT 204
Db 878 CACTTTCCCAATTGCTTTTGT 901

RESULT 6
AF304333

```





ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 3032)  
AUTHORS Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and  
Dharmarajan, A.M.  
TITLE Cloning, characterization and regulation of an inhibitor of  
apoptosis protein in the rat corpus luteum  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3032)  
AUTHORS Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2000) Anatomy and Human Biology, University of  
Western Australia, Verduin St, Nedlands, WA 6907, Australia  
FEATURES  
source Location/Qualifiers  
1..3032  
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BASE COUNT 817 a 657 c 688 g 870 t

ORIGIN  
Query Match 87.5%; Score 178.4; DB 10; Length 3032;  
Best Local Similarity 92.2%; Pred. No. 3.4e-44;  
Matches 188; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGCAAGTCAATTCAGAACTGGCGGCGACTATGCTCATTTAACCCCCAGA 60  
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QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGCGCTGATGATCAAGTCAATGCTTTGT 120  
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DB 1472 GAGTTAGCTAGTGGCTCTACTACACAGGCGCTGATGATCAAGTCAATGCTTTGT 1531  
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QY 121 TGTGGGGAAACAGAAAATTTGGAAACCTGTGATCGCTGGCTGAGAACACAGGAGA 180  
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DB 1532 TGTGGTGAACAGAAAATTTGGAAACCTGTGACCGCTGCTGCTGAGAACACAGGAGA 1591  
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QY 181 CACTTCCCAATGCTTTTGT 204  
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DB 1592 CACTTCCCAATGCTTTTGT 1615  
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RESULT 9  
AF183429  
LOCUS Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete  
DEFINITION cds.  
ACCESSION AF183429  
VERSION AF183429.1 GI:10765280  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORGANISM Rattus norvegicus  
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 1491)  
AUTHORS Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.  
TITLE Cloning and characterization of the rat homologues of the Inhibitor  
of Apoptosis protein 1, 2, and 3 genes  
JOURNAL BMC Genomics 3 (1), 5 (2002)  
PUBMED 11860601  
REFERENCE 2 (bases 1 to 1491)  
AUTHORS Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-1999) Department of Biochemistry, Microbiology  
and Immunology, University of Ottawa, 451 Smyth Road, Ottawa,  
Ontario K1H 8M5, Canada  
FEATURES  
source Location/Qualifiers  
1..1491  
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/codon\_start=1  
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EHRHFPNFFVLRNVRSESGVSSDRNFPNSTSPNPRMAEYDARIYVFTGWL  
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BASE COUNT 464 a 282 c 357 g 388 t

ORIGIN  
Query Match 86.7%; Score 176.8; DB 10; Length 1491;  
Best Local Similarity 91.7%; Pred. No. 1.1e-43;  
Matches 187; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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DB 487 GAAGAAGCCAGATTGCAAGTCAATTCAGAACTGGCGGCGACTATGCTCATTTAACCCCCAGA 546  
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QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGCGCTGATGATCAAGTCAATGCTTTGT 120  
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DB 547 GAGTTAGCTAGTGGCTCTACTACACAGGCGCTGATGATCAAGTCAATGCTTTGT 606  
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QY 121 TGTGGGGAAACAGAAAATTTGGAAACCTGTGATCGCTGGCTGAGAACACAGGAGA 180  
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DB 607 TGTGGTGAACAGAAAATTTGGAAACCTGTGACCGCTGCTGCTGAGAACACAGGAGA 666  
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QY 181 CACTTCCCAATGCTTTTGT 204  
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DB 667 CACTTCCCAATGCTTTTGT 690  
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RESULT 10  
E31042  
LOCUS Method for screening substance inhibiting binding to XIAP.  
DEFINITION E31042  
ACCESSION E31042  
VERSION E31042.1 GI:13017307  
KEYWORDS JP 1999326328-A/2.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1659)  
AUTHORS Kunihiro, M.  
TITLE Method for screening substance inhibiting binding to XIAP  
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;  
KUNIHIRO MATSUMOTO  
COMMENT OS Unidentified





	Matches	184;	Conservative	0;	Mismatches	20;	Indels	0;	Gaps	0;
Qy	1	GAAGAAGCCAGATGAAGTCATTTCAGAACTGGCGGACATATGCTCATTTTAAACCCCAGA	60							
Db	520	GAGAAGCTAGATAAAGTCCTTTCAGAACTGGCGCAACTATGCTCACCTAACCCCCAGA	579							
Qy	61	GAGTTAGCTAGTGTCGCCCTCTACTACAGAGGGCCTGATGATCAAGTGCATGTCTTTGT	120							
Db	580	GAGTTAGCAAGTGTGGTAGCTCTACTACACAGGTATTGTGACCAAAGTCAGTCTTTGT	639							
Qy	121	TGTGGGGGAAAACATGAAAAATTGGGAACCTGTGATCGTCCTGGTCAGACACACAGAGA	180							
Db	640	TGTGGTGAAAACATGAAAAATTGGGAACCTGTGATCGTCCTGGTCAGACACACAGAGA	699							
Qy	181	CACHTTCCCAATTGCTTTTTTTTGT	204							
Db	700	CACHTTCCCTAATTGCTTCTTTTGT	723							

Search completed: April 15, 2003, 23:25:29  
Job time : 1035.86 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 136.354 Seconds

(without alignments)  
3369.223 Million cell updates/sec

Title: US-09-654-743-50  
Perfect score: 204  
Sequence: 1 gaagaagccagattgaagtc.....ttcccaattgctttttgtt 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	18 AAT70839	Mouse apoptosis in
2	204	100.0	2100	24 ABK93872	Mouse cDNA encodin
3	204	100.0	2691	19 AAV55041	Murine XIAP coding
4	202.4	99.2	1988	18 AAT72710	Mouse inhibitor of
5	172	84.3	1659	21 AAZ48862	Human XIAP coding
6	172	84.3	2540	18 AAT70836	Human apoptosis in
7	172	84.3	2540	21 AAA64901	Human X-linked inh
8	172	84.3	2540	24 ABK93869	Human cDNA encodin
9	172	84.3	3000	24 ABK93875	Human cDNA encodin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

10	172	84.3	5232	19 AAV55038	Human XIAP coding
11	161	78.9	2404	24 AAK99405	DNA of APP related
12	156	76.5	1758	24 ABK14677	Human Inhibitor of
13	154.4	75.7	1559	24 ABK13197	Human testes speci
14	154.4	75.7	1758	24 ABK14678	Human inhibitor of
15	154.4	75.7	4993	22 AAD03581	Human IAP-like pro
16	120.8	59.2	7990	24 ABL54307	Chemically treated
17	120.8	59.2	7990	24 ABL32158	Human immune syste
18	103.8	50.9	7990	24 ABL54308	Chemically treated
19	103.8	50.9	7990	24 ABL32159	Human immune syste
20	81.4	39.9	2601	18 AAT61591	Human c-IAP2. Hom
21	81.4	39.9	2666	18 AAT70837	Human apoptosis in
22	81.4	39.9	2676	24 ABK93870	Human cDNA encodin
23	81.4	39.9	3076	18 AAT72712	Human inhibitor of
24	81.4	39.9	3076	20 AAZ41005	Human cellular inh
25	81.4	39.9	3076	20 AAZ22096	Human cellular inh
26	81.4	39.9	3076	24 ABL62746	Breast cancer rela
27	81.4	39.9	3076	24 ABL66325	Lung cancer relate
28	81.4	39.9	3734	22 AAC90972	Human API2-MIT chi
29	81.4	39.9	3734	24 ABK52387	DNA encoding cysti
30	81.4	39.9	6669	19 AAV55039	Human HIAP-1 codin
31	81.4	39.9	6669	24 ABK93876	Human cDNA encodin
32	72.8	35.7	2862	18 AAT61592	Murine c-IAP. Mus
33	72.8	35.7	3151	19 AAV55043	Murine HIAP-2 codi
34	71.8	35.2	2291	22 AAS06025	Angiotensin conver
35	71.8	35.2	2580	18 AAT70838	Human apoptosis in
36	71.8	35.2	2580	24 ABK93871	Human cDNA encodin
37	71.8	35.2	2580	18 AAT61590	Human c-IAP1. Hom
38	71.8	35.2	3532	18 AAT72711	Human inhibitor of
39	71.8	35.2	3532	20 AAZ22143	Human cellular inh
40	71.8	35.2	3532	24 ABK96857	Gene #3355 used to
41	71.8	35.2	3732	19 AAV55040	Human HIAP-2 codin
42	71.2	34.9	2416	18 AAT70841	Mouse apoptosis in
43	71.2	34.9	2416	24 ABK93874	Mouse cDNA encodin
44	70.2	34.4	1435	17 AAT43709	Human inhibitor of
45	63	30.9	2474	18 AAT70840	Mouse apoptosis in

#### ALIGNMENTS

RESULT 1  
AAT70839  
ID AAT70839 standard; cDNA; 2100 BP.  
AC AAT70839;  
XX  
XX  
DT 02-SEP-1997 (first entry)  
XX  
DE Mouse apoptosis inhibitor m-xiap cDNA.  
XX  
XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;  
KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
KW Ischaemia; myocardial infarction; stroke;  
KW reperfusion injury; toxin-induced liver disease; gene therapy;  
KW diagnosis; ds.  
XX  
XX Mus sp.  
OS  
FH Key  
CDS Location/Qualifiers  
FT 127..1617  
FT /\*tag= a  
XX  
PN WO9706255-A2.  
XX  
XX 20-FEB-1997.  
XX  
XX 05-AUG-1996; 96WO-IB01022.  
XX  
XX 22-DEC-1995; 95US-0576956.  
PR 04-AUG-1995; 95US-0511485.  
XX  
XX (UYOT-) UNIV OTTAWA.

XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;  
 XX PA WPI; 1997-154262/14.  
 DR P-PSDB; AAW19584.  
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
 PT of susceptibility to apoptotic disease  
 XX Claim 11; Page 78-79; 219pp; English.  
 XX Human XIAP, hiap-1 and hiap-2 genes, and murine XIAP, hiap-1 and  
 CC hiap-2 genes (AA70836-41) respectively code for a new class of  
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis  
 CC (IAP). The murine XIAP gene (for X-linked IAP gene) sequence was  
 CC constructed from 12 overlapping clones isolated from a mouse  
 CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic  
 CC library using human XIAP cDNA as probe. IAP nucleic acids can be  
 CC used to express IAP polypeptides in cells and animals to inhibit  
 CC apoptosis, and as primers and probes to identify and isolate  
 CC additional IAP genes, as well as in methods for treating diseases  
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).  
 XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;  
 SQ Query Match 100.0%; Score 204; DB 18; Length 2100;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-61;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGAAGCCAGATGAGTCAATTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 60  
 Db 613 GAAGAAGCCAGATGAGTCAATTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 672  
 QY 61 GAGTTAGTCTAGTGGCTCTACTACAGAGGCGCTGATGATCAAGTCAATGCTTTTGT 120  
 Db 673 GAGTTAGTCTAGTGGCTCTACTACAGAGGCGCTGATGATCAAGTCAATGCTTTTGT 732  
 QY 121 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATCGTGGTGCAGACACAGGAGA 180  
 Db 733 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATCGTGGTGCAGACACAGGAGA 792  
 QY 181 CACTTTCCCAATGCTTTTGT 204  
 Db 793 CACTTTCCCAATGCTTTTGT 816  
 RESULT 2  
 ABK93872  
 ID ABK93872 standard; cDNA; 2100 BP.  
 XX AC ABK93872;  
 XX 26-AUG-2002 (first entry)  
 XX Mouse cDNA encoding inhibitor of apoptosis, XIAP.  
 DE Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX OS Mus sp.  
 XX WO200226968-A2.  
 XX 04-APR-2002.  
 XX 27-SEP-2001; 2001WO-CA01379.  
 XX 28-SEP-2000; 2000US-0672717.

XX (UYOT-) UNIV OTTAWA.  
 PA (AEGE-) AEGERA THERAPEUTICS INC.  
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 PI WPI; 2002-479562/51.  
 XX DR P-PSDB; ABG65666.  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX Disclosure; Fig 4; 135pp; English.  
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP  
 CC cDNA sequence.  
 XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;  
 SQ Query Match 100.0%; Score 204; DB 24; Length 2100;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-61;  
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGAAGCCAGATGAGTCAATTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 60  
 Db 613 GAAGAAGCCAGATGAGTCAATTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 672  
 QY 61 GAGTTAGTCTAGTGGCTCTACTACAGAGGCGCTGATGATCAAGTCAATGCTTTTGT 120  
 Db 673 GAGTTAGTCTAGTGGCTCTACTACAGAGGCGCTGATGATCAAGTCAATGCTTTTGT 732  
 QY 121 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATCGTGGTGCAGACACAGGAGA 180  
 Db 733 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATCGTGGTGCAGACACAGGAGA 792  
 QY 181 CACTTTCCCAATGCTTTTGT 204  
 Db 793 CACTTTCCCAATGCTTTTGT 816  
 RESULT 3  
 AAV55041  
 ID AAV55041 standard; cDNA; 2691 BP.  
 XX AC AAV55041;  
 XX 13-NOV-1998 (first entry)  
 XX Murine XIAP coding sequence.  
 DE Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.  
 XX Mus sp.  
 XX Key Location/Qualifiers  
 FH

```

FT CDS          672...2162
FT              /*tag= a
FT              /product= XIAP
XX WO9835693-A2.
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-IB00781.
XX 13-FEB-1997; 97US-0800929.
XX (UYOT-1) UNIV OTTAWA.
XX
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX
XX WPI; 1998-467164/40.
XX P-PSDB; AAW69297.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX presence of IAP and NAIP, specifically applied to cancers involving
XX p53 mutations
XX
XX Claim 13; Fig 4; 147pp; English.
XX
XX This sequence encodes the mouse XIAP protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors.
XX
XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;
XX
XX
XX Query Match          100.0%; Score 204; DB 19; Length 2691;
XX Best Local Similarity 100.0%; Pred. No. 1,2e-61;
XX Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAGAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAACCCCCAGA 60
XX |||||||
XX DB 1158 GAAGAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAACCCCCAGA 1217
XX |||||||
XX QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTGT 120
XX |||||||
XX DB 1218 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTGT 1277
XX |||||||
XX QY 121 TGTGGGGGAAACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 180
XX |||||||
XX DB 1278 TGTGGGGGAAACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 1337
XX |||||||
XX QY 181 CACTTTCCCAATTGCTTTTGT 204
XX |||||||
XX DB 1338 CACTTTCCCAATTGCTTTTGT 1361
XX |||||||
XX
XX RESULT 4
XX AAT72710
XX ID AAT72710 standard; DNA; 1988 BP.
XX AC AAT72710;
XX XX
XX DT 16-SEP-1997 (first entry)

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XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
XX degenerative disease; infectious disease; autoimmune disease;
XX cancer; gene therapy; diagnosis; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 212..1702
XX /*tag= a
XX
XX WO9723501-A1.
XX 03-JUL-1997.
XX
XX 20-DEC-1996; 96WO-AU00827.
XX
XX 22-DEC-1995; 95AU-0007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI; 1997-350966/32.
XX P-PSDB; AAW19745.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX to modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer
XX
XX Claim 24; Page 44-47; 136pp; English.
XX
XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse
XX liver cDNA library on the basis of homology to Orgyia pseudotsugata
XX polyhedrosis virus IAP BIR and RING finger amino acid motifs.
XX Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
XX to produce polypeptides useful in methods for modulating apoptosis
XX in animal cells, specifically for treatment, by inhibition, of
XX degenerative and infectious disease or, by promotion, of cancer and
XX autoimmune disease, and can be used for gene therapy of these
XX diseases.
XX
XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
XX
XX
XX Query Match          99.2%; Score 202.4; DB 18; Length 1988;
XX Best Local Similarity 99.5%; Pred. No. 4e-61;
XX Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GAAGAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAACCCCCAGA 60
XX |||||||
XX DB 698 GAAGAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAACCCCCAGA 757
XX |||||||
XX QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTGT 120
XX |||||||
XX DB 758 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTGT 817
XX |||||||
XX QY 121 TGTGGGGGAAACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 180
XX |||||||
XX DB 818 TGTGGGGGAAACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 877
XX |||||||
XX QY 181 CACTTTCCCAATTGCTTTTGT 204
XX |||||||
XX DB 878 CACTTTCCCAATTGCTTTTGT 901
XX |||||||
XX
XX RESULT 5
XX AA248862
XX ID AA248862 standard; cDNA; 1659 BP.
XX XX

```



AA248862;  
 24-MAR-2000 (first entry)  
 Human XIAP coding sequence.  
 Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; transforming growth factor-beta; ds.  
 Homo sapiens.  
 JPL1326328-A.  
 26-NOV-1999.  
 13-MAY-1998; 98JP-0130378.  
 13-MAY-1998; 98JP-0130378.  
 (MATS/) MATSUMOTO K.  
 WPI; 2000-078337/07.  
 P-PSDB; AAY59451.  
 Screening a substance which inhibits combination of the X-linked inhibitor of apoptosis protein -  
 Disclosure; Page 28-30; 43pp; Japanese.  
 This sequence encodes the human XIAP protein.  
 The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1 (TAK1) binding protein 1 (TAB1) and a substance to be tested are contacted with each other and then the presence or formation of a complex between XIAP and TAB1 is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta (Transforming growth factor-beta) type I and/or type II receptor is useful as a drug.  
 Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
 Query Match 84.3%; Score 172; DB 21; Length 1659;  
 Best Local Similarity 90.2%; Pred. No. 2.1e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 GAAGAACCCAGATTGAAGTCTATTTCAGAACTGGCCGACACTATGCTCACTTTAACCCCCAGA 60  
 DB 568 GAAGAACTAGATTAAAGTCTCTTTTCAGAACTGGCCGACACTATGCTCACTTAACCCCAAGA 627  
 QY 61 GAGTTAGTCTAGTGTGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120  
 DB 628 GAGTTAGCAAGTGTGCACTACTACACAGGTATTGTTGACCAAGTGCAGTGTGTTGT 687  
 QY 121 TGTGGGGAAACATGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGAGA 180  
 DB 688 TGTGGTGGAAACATGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGCGGA 747  
 QY 181 CACTTTCCCAATTCCTTTTGT 204  
 DB 748 CACTTTCCCAATTCCTTTTGT 771  
 RESULT 6  
 AAT70836  
 ID AAT70836 standard; cDNA; 2540 BP.  
 XX

AAT70836;  
 02-SEP-1997 (first entry)  
 Human apoptosis inhibitor xiap cDNA.  
 Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis; ds.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 34..1527  
 FT /\*tag= a  
 WC9706255-A2.  
 20-FEB-1997.  
 05-AUG-1996; 96WO-1B01022.  
 22-DEC-1995; 95US-0576956.  
 04-AUG-1995; 95US-0511485.  
 (UYOT-) UNIV OTTAWA.  
 Baird S, Korneluk RG, Liston P, Mackenzie AE;  
 WPI; 1997-154262/14.  
 P-PSDB; AAW19581.  
 Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease  
 Claim 12; Page 67-68; 219pp; English.  
 Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2 genes (AAT70836-41) respectively code for a new class of mammalian proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII cDNA library using an X-linked sequence tag site that shows strong homology with the conserved ring zinc finger domain of baculovirus CpiAP and OpiAP genes. The gene was assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases and disorders involving apoptosis (anti-apoptotic gene therapy).  
 Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;  
 Query Match 84.3%; Score 172; DB 18; Length 2540;  
 Best Local Similarity 90.2%; Pred. No. 2.5e-50;  
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 GAAGAACCCAGATTGAAGTCTATTTCAGAACTGGCCGACACTATGCTCACTTTAACCCCCAGA 60  
 DB 520 GAAGAACTAGATTAAAGTCTCTTTTCAGAACTGGCCGACACTATGCTCACTTAACCCCAAGA 579  
 QY 61 GAGTTAGTCTAGTGTGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120  
 DB 580 GAGTTAGCAAGTGTGCACTACTACACAGGTATTGTTGACCAAGTGCAGTGTGTTGT 639  
 QY 121 TGTGGGGAAACATGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGAGA 180  
 DB 640 TGTGGTGGAAACATGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGCGGA 699  
 QY 181 CACTTTCCCAATTCCTTTTGT 204







XX PF 18-JUL-2001; 2001WO-EP08287.  
 XX PR 28-JUL-2000; 2000EP-0116452.  
 XX PA (MERE ) MERCK PATENT GMBH.  
 XX PI Hentsch B;  
 XX DR WPI; 2002-188741/24.  
 XX DR P-PSDB; AAU75747.  
 XX PT New inhibitor of apoptosis proteins and polynucleotides useful in  
 PT vaccines for inducing an immune response against hyperproliferative  
 PT diseases e.g. cancer  
 XX PS Claim 5; Page 33-35; 41pp; English.  
 XX CC This invention relates to the nucleic acid and protein sequences of a  
 CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences  
 CC have homology to the IAP (inhibitors of apoptosis) gene family which  
 CC are thought to inhibit proteins by regulating the anti-apoptotic  
 CC activity of the V-rel and NF-kappaB family of transcription factors.  
 CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids  
 CC of the invention are useful for screening to identify compounds that  
 CC stimulate or inhibit the function or level of IAPL7, where the  
 CC identified compounds are useful for treating hyper-proliferative  
 CC diseases such as cancer. The protein sequences may also be used to  
 CC identify membrane bound or soluble receptors of IAPL7 by standard  
 CC receptor binding techniques. Nucleic acids encoding IAPL7, may be used  
 CC as hybridisation probes for cDNA and genomic DNA, or as primers for  
 CC nucleic acid amplification reaction and the primers and probes may also  
 CC be used to isolate full-length cDNAs and genomic clones encoding IAPL7.  
 CC The nucleic acid sequences are useful as diagnostic reagents for  
 CC diagnosing a disease or a susceptibility to a disease by detecting  
 CC mutations in the associated gene. The nucleic acid sequence is useful  
 CC for chromosome localisation and tissue expression studies and is also  
 CC useful for producing transgenic animals. The IAPL7 protein sequence may  
 CC also be used to generate an anti-IAPL7 antibody which is useful in  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and protein in cells. The sequences of the invention  
 CC are also useful as vaccines for inducing an immunological response in a  
 CC mammal. The present sequence represents the cDNA encoding the human  
 CC inhibitor of apoptosis 7 (IAP7) protein of the invention.  
 XX SQ Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;  
 Query Match 76.58; Score 156; DB 24; Length 1758;  
 Best Local Similarity 85.34; Pred. No. 9.9e-45;  
 Matches 174; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 GAAGAAGCCAGATTGAAGTTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 60  
 DB 673 GAAGAAGCTAGATTACAGTGTTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 732  
 QY 61 GAGTACCTAGTGTGCTGCTTACTACACAGGGGCTGATGATCAAGTGCATGCTTTGT 120  
 DB 733 GAGCTGGCAGTGTGGCTGTACTACACAGGCACTGATGACCAAGTGCAGTGTCTGT 792  
 QY 121 TGTGGGGAAACAGAAAATTTGGAAACCTGTGATCGTGGTGTGAGAACACAGAGA 180  
 DB 793 TGTGGCGGAAACAGAAAATTTGGAAACCTGTGATCGTGGTGTGAGAACACAGAGA 852  
 QY 181 CACTTTCCTCAATGCTTTTGT 204  
 DB 853 CATTTCCTCAATGCTTTTATT 876

RESULT 13  
 ABK13197  
 ID ABK13197 standard; DNA; 1559 BP.  
 XX AC ABK13197;

XX DT 23-APR-2002 (first entry)  
 XX DE Human testes specific inhibitor of apoptosis (TIAP) gene.  
 XX KW TIAP; apoptosis; testes specific inhibitor of apoptosis; gene;  
 KW human; ds; apoptotic; cytostatic; anti-infertility; contraceptive;  
 KW chromosome 12q22-23; transgenic animal; antibody; immunogen;  
 KW testicular cell; testicular cancer; cancer; male infertility;  
 KW male birth control; XIAP.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 791..1501  
 FT /tag- a  
 FT /product= "TIAP protein"  
 XX PN US6331412-B1.  
 XX PD 18-DEC-2001.  
 XX PF 29-JAN-1999; 99US-0239867.  
 XX PR 29-JAN-1998; 98US-073001P.  
 XX PA (UYOT-) UNIV OTTAWA.  
 XX PI Korneluk RG, Lagace M;  
 XX WPI; 2002-105275/14.  
 XX DR P-PSDB; AAU75066.  
 XX CC Nucleic acids encoding a testis specific apoptosis inhibitor protein  
 CC (TIAP) useful for treating testicular cancers, cancers in  
 CC non-testicular tissues, male infertility, and for achieving male birth  
 CC control  
 XX PS Claim 2; Fig 4A; 29pp; English.  
 XX CC This invention relates to a novel isolated nucleic acid molecule  
 CC encoding a TIAP polypeptide (testes-specific inhibitor of apoptosis)  
 CC protein. This gene is a homologue of the X-linked XIAP gene and is  
 CC located on chromosome 12q22-23. The nucleotide and protein sequences of  
 CC the invention and vectors containing these sequences may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate TIAP expression. Additionally, the nucleotide sequence may  
 CC be used to express the TIAP protein by recombinant methods. Conversely,  
 CC antisense nucleic acid molecules may be administered to down-regulate  
 CC TIAP expression. The nucleotide sequence, may also be used to design DNA  
 CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to  
 CC detect and quantitate the presence of similar nucleic acid sequences in  
 CC samples, to identify patients who may be in need of restorative therapy.  
 CC Through the production of transgenic animals and cells, the sequences  
 CC may also be used to study the expression and function of TIAP proteins  
 CC and their role in metabolism. The TIAP polypeptides may be used to  
 CC produce antibodies against TIAP and maybe used to identify modulators  
 CC (agonists and antagonists) of TIAP expression and activity. An anti-TIAP  
 CC antibody or antagonist may also be used to down-regulate TIAP expression  
 CC and activity. The reagents may be used in this way for the treatment of  
 CC excessive or insufficient apoptosis, particularly in testicular cells.  
 CC In particular they are useful in diagnosing and treating testicular  
 CC cancers, cancers in non-testicular tissues, male infertility, and for  
 CC achieving male birth control. The present sequence represents the  
 CC human TIAP gene sequence of the invention.  
 XX SQ Sequence 1559 BP; 465 A; 309 C; 396 G; 387 T; 2 other;  
 Query Match 75.78; Score 154.4; DB 24; Length 1559;  
 Best Local Similarity 84.88; Pred. No. 3.5e-44;  
 Matches 173; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTTCAGAACTGGCGGACATGCTCATTTAAACCCCGAGA 60



XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Duckett C, Mir SS;  
XX WPI: 2001-258135/26.  
DR P-PSDB; AAE00365.  
XX  
PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with  
PT transforming growth factor beta receptor modulating activity, and the  
PT nucleic acids that encode them, useful for treating, e.g. diabetes and  
PT multiple sclerosis  
XX  
PS Claim 18; Page 94-98; 108pp; English.  
XX  
CC The present sequence is human inhibitor of apoptosis (IAP)-like protein-2  
CC (ILP-2) cDNA. The hILP-2 gene is located on chromosome 19q13.3-q13.4.  
CC ILP-2 comprises a single amino-terminal domain known as baculovirus iap  
CC repeat (BIR), followed by a spacer region and a carboxy-terminal ring  
CC finger domain. It interacts with transforming growth factor beta  
CC receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially  
CC inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and  
CC Apaf-1. It also activates c-Jun N-terminal Kinase (JNK) activity. ILP-2  
CC is used in the area of genetic testing for predisposition to diseases,  
CC such as cone-rod retinal dystrophy-2, retinitis pigmentosa,  
CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer  
CC and hyperferritinemia-catact syndrome owing to an ILP-2 deletion or  
CC mutation. The ILP is also used in the treatment of diseases associated  
CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,  
CC diabetes and multiple sclerosis and neurodegenerative diseases including  
CC retinal degeneration. The ILP-2 gene is also used in gene therapy for  
CC treating patients suffering from ILP-2 gene deletions or mutations.  
XX  
SQ Sequence 4993 BP: 1526 A; 973 C; 1196 G; 1297 T; 1 other:  
Query Match 75.7%; Score 154.4; DB 22; Length 4993;  
Best Local Similarity 84.8%; Pred. No. 5.7e-44;  
Matches 173; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGACTATGCTCATTTAAACCCCGAGA 60  
Db 1777 GAAGAAGCTAGATAACAGTCGTTTCACAACTGCCAGCCTCTGCCACCTTGACCCCGAGA 1836  
QY 61 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGCTGATGATCAAGTCGCTTTCT 120  
Db 1837 GAGCTGGCCAGTCTGGGCTGTACTACACAGGCACTGATGACCAAGTCAGTCTCTCT 1896  
QY 121 TGTGGGGGAAACTGAAATTTGGAAACCTGTGATCGTGGCTGGTCAGACACAGGAGA 180  
Db 1897 TGTGGCGGAAACTGAAATTTGGAAACCTGTGATCGTGGCTGGTCAGACACAGGAGA 1956  
QY 181 CACTTTCCCAATTGCTTTTGT 204  
Db 1957 CATTTCCTAATGCTTCTTATT 1980  
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Job time : 139.354 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 25.6771 Seconds  
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	204	100.0	2100	2	US-08-511-485-9
2	204	100.0	2691	3	US-09-212-971-9
3	204	100.0	2691	3	US-08-800-929A-9
4	204	100.0	2691	4	US-09-617-053A-9
5	172	84.3	1588	4	US-09-239-867-3
6	172	84.3	2540	2	US-08-511-485-3
7	172	84.3	2540	3	US-09-392-580-1
8	172	84.3	5232	3	US-09-212-971-3
9	172	84.3	5232	3	US-08-800-929A-3
10	172	84.3	5232	4	US-09-617-053A-3
11	154.4	75.7	1559	4	US-09-239-867-1
12	81.4	39.9	2601	4	US-08-569-749-3
13	81.4	39.9	2601	5	PCT-US96-12860-3
14	81.4	39.9	2675	5	US-08-511-485-5
15	81.4	39.9	3075	2	US-09-205-144-1
16	81.4	39.9	6669	3	US-09-212-971-5
17	81.4	39.9	6669	3	US-08-800-929A-5
18	81.4	39.9	6669	4	US-09-617-053A-5
19	72.8	35.7	2862	4	US-08-569-749-13
20	72.8	35.7	2862	5	PCT-US96-12860-13
21	72.8	35.7	3151	3	US-09-212-971-13
22	72.8	35.7	3151	3	US-08-800-929A-13
23	72.8	35.7	3151	4	US-09-617-053A-13
24	71.8	35.2	2580	2	US-08-511-485-7
25	71.8	35.2	2589	4	US-08-569-749-1
26	71.8	35.2	2589	5	PCT-US96-12860-1
27	71.8	35.2	3532	2	US-09-205-204-1

28	71.8	35.2	3732	3	US-09-212-971-7	Sequence 7, Appli
29	71.8	35.2	3732	3	US-08-800-929A-7	Sequence 7, Appli
30	71.8	35.2	3732	4	US-09-617-053A-7	Sequence 7, Appli
31	70.2	34.4	1435	5	PCT-US95-05922A-1	Sequence 1, Appli
32	63	30.9	2676	3	US-09-212-971-11	Sequence 11, Appli
33	63	30.9	2676	3	US-08-800-929A-11	Sequence 11, Appli
34	63	30.9	2676	4	US-09-617-053A-11	Sequence 11, Appli
35	54.2	26.6	5502	3	US-08-836-134-1	Sequence 1, Appli
36	54.2	26.6	5502	4	US-09-493-784-1	Sequence 1, Appli
37	41.2	20.2	711	3	US-09-121-979-3	Sequence 3, Appli
38	41.2	20.2	711	4	US-09-332-319-3	Sequence 3, Appli
39	35.6	17.5	176373	3	US-09-128-155-17	Sequence 17, Appli
40	34.8	17.1	152331	3	US-09-128-155-16	Sequence 16, Appli
41	32.8	16.1	436	2	US-08-824-701A-7	Sequence 7, Appli
42	29.2	14.3	1400	2	US-08-001-078A-2	Sequence 2, Appli
43	29.2	14.3	1400	2	US-08-463-218-2	Sequence 2, Appli
44	29.2	14.3	1400	5	PCT-US94-00253-2	Sequence 2, Appli
45	28.2	13.8	10614	1	US-08-135-511-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1  
US-08-511-485-9  
; Sequence 9, Application US/08511485  
; Patent No. 5919912  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/511.485  
; FILING DATE: 04-AUG-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 07540/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2100 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: DNA (genomic)  
US-08-511-485-9

Query Match 100.0%; Score 204; Length 2100;  
Best Local Similarity 100.0%; Pred. No. 5.9e-62;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCCGCGACTATGCTATTAAACCCCGAGA 60  
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Db 613 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGACTATGCTCATTTTAACCCCGAGA 672  
QY 61 GAGTAGTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTGT 120  
Db 673 GAGTTAGTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTGT 732  
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCTGGTGCAGAACACAGGAGA 180  
Db 733 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCTGGTGCAGAACACAGGAGA 792  
QY 181 CACTTTCCCAATGCTTTTGT 204  
Db 793 CACTTTCCCAATGCTTTTGT 816

## RESULT 2

US-09-212-971-9  
; Sequence 9, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; EARLIER FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2691  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-212-971-9

Query Match 100.0%; Score 204; DB 3; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 6.5e-62;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGACTATGCTCATTTTAACCCCGAGA 60  
Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGACTATGCTCATTTTAACCCCGAGA 1217  
QY 61 GAGTAGTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTGT 120  
Db 1218 GAGTTAGTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTGT 1277  
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCTGGTGCAGAACACAGGAGA 180  
Db 1278 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCTGGTGCAGAACACAGGAGA 1337  
QY 181 CACTTTCCCAATGCTTTTGT 204  
Db 1338 CACTTTCCCAATGCTTTTGT 1361

## RESULT 3

US-08-800-929A-9  
; Sequence 9, Application US/08800929A  
; Patent No. 613437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Ebling LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,929A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,590  
; FILING DATE: 14-NOV-1996  
; APPLICATION NUMBER: 60/017,354  
; FILING DATE: 26-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bleker-Brady, Kristina  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 07891/009001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2691 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-800-929A-9

Query Match 100.0%; Score 204; DB 3; Length 2691;  
Best Local Similarity 100.0%; Pred. No. 6.5e-62;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGACTATGCTCATTTTAACCCCGAGA 60  
Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGACTATGCTCATTTTAACCCCGAGA 1217  
QY 61 GAGTAGTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTGT 120  
Db 1218 GAGTTAGTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTGT 1277  
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCTGGTGCAGAACACAGGAGA 180  
Db 1278 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCTGGTGCAGAACACAGGAGA 1337  
QY 181 CACTTTCCCAATGCTTTTGT 204  
Db 1338 CACTTTCCCAATGCTTTTGT 1361

## RESULT 4

US-09-617-053A-9  
; Sequence 9, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:

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; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match      100.0%; Score 204; DB 4; Length 2691;
Best Local Similarity 100.0%; Pred. No. 6.5e-62;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGGCTGATGATCAATTAACCCCCAGA 60
DB 1158 GAAGAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGGCTGATGATCAATTAACCCCCAGA 1217
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 120
DB 1218 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 1277
QY 121 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGTGATGATCAAGTGAATGCTTTTGT 180
DB 1278 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGTGATGATCAAGTGAATGCTTTTGT 1337
QY 181 CACTTTCCCAATGCTTTTGT 204
DB 1338 CACTTTCCCAATGCTTTTGT 1361

RESULT 5
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match      84.3%; Score 172; DB 4; Length 1588;
Best Local Similarity 90.2%; Pred. No. 8.7e-51;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGGCTGATGATCAATTAACCCCCAGA 60
DB 520 GAAGAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGGCTGATGATCAATTAACCCCCAGA 579
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 120
DB 580 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 639
QY 121 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGTGATGATCAAGTGAATGCTTTTGT 180
DB 640 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGTGATGATCAAGTGAATGCTTTTGT 699
QY 181 CACTTTCCCAATGCTTTTGT 204

Query Match      84.3%; Score 172; DB 2; Length 2540;
Best Local Similarity 90.2%; Pred. No. 1e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGGCTGATGATCAATTAACCCCCAGA 60
DB 520 GAAGAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGGCTGATGATCAATTAACCCCCAGA 579
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 120
DB 580 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 639
QY 121 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGTGATGATCAAGTGAATGCTTTTGT 180
DB 640 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGTGTGATGATCAAGTGAATGCTTTTGT 699
QY 181 CACTTTCCCAATGCTTTTGT 204
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REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Other
LOCATION: 1...5232
OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.
US-08-800-929A-3

Query Match      84.3%; Score 172; DB 3; Length 5232;
Best Local Similarity 90.2%; Pred. No. 1.4e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGGACTATGCTCATTTAACCCCCAGA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 520 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCGGAGACTATGCTCATTTAACCCCAAGA 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 580 GAGTTAGCAAGTCGCGACTCTACTACACAGGATTTGGTACCAAGTGGAGTGGCTTTGT 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGGGGAAACACTGAAAAATTTGGAAACCTGTGATCGTCTGCTGAGAACACAGGAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 640 TGTGGTGAACAACTGAAAAATTTGGAAACCTGTGATCGTCTGCTGAGAACACAGGCGA 699
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CACTTTCCTAATGCTTTTGT 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 700 CACTTTCCTAATGCTTTTGT 723
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-239-867-1
; Sequence 1, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(1559)
; OTHER INFORMATION: n = A,T,C or G
US-09-239-867-1

Query Match      75.7%; Score 154.4; DB 4; Length 1559;
Best Local Similarity 84.8%; Pred. No. 1.3e-44;
Matches 173; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGGACTATGCTCATTTAACCCCCAGA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 494 GAAGAAGCTAGATAACAGTCGTTTCACAACTGGCCAGCCTCTGCCACTTGACCCCGAGA 553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 554 GAGCTGGCCAGTGGCTGGCTGACTACACAGGCACTGATGACCAAGTGGAGTGGCTTCTGT 613
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGGGGAAACACTGAAAAATTTGGAAACCTGTGATCGTCTGCTGAGAACACAGGAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 614 TGTGGCGAAACACTGAAAAATTTGGAAACCTGGTGTGATCGTCTGCTGAGAACACAGGAGA 673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CACTTTCCTAATGCTTTTGT 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 674 CACTTTCCTAATGCTTTTGT 697
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-08-569-749-3
; Sequence 3, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
```

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/12860
: FILING DATE: 06 AUG 1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U. S. Serial Nos. 08/512,944
: CLASSIFICATION:
: INVENTOR/AGENT INFORMATION:

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NAME/REGISTRATION INFORMATION:  
REGISTRATION NUMBER: 24, 774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US96-12850-3

Query Match          39.9%; Score 81.4; DB 5;
Best Local Similarity 66.0%; Pred. No. 5.9e-19;
Matches 134; Conservative 0; Mismatches -66;

QY      1  GAGANGCCAGATTGAAGTCATTTCAGAACTGCCCGGACTATGCC
      |||  |||||  |||  |||||  |||||  |||||  |||||  |||||
DB      627  GAAATGCCAGATTACTTACTTTTCAGACATGCC---ATTGAC

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Db 684 GATCTGGCAAGCAGGCTTTTACATACGACCTGGAGACAGG  
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCCCTGTGTCTGTGCTGTG

DB	744	TCGGTGGAAATGACCAATTGGGAACCGCAGGATTAATGCTAT
QY	181	CACCTTCCCAATGCTTTTTTGT 203
DB	804	CATTTCCTCCCAATGCCCATTTAT 826

RESULT 14  
 US-08-511-485-5  
 : Sequence 5, Application US/08511485  
 : Patent No. 5919912

; GENERAL INFORMATION:  
 ; APPLICANT: Korneluk, Robert G.  
 ; APPLICANT: Mackenzie, Alexander E.  
 ; APPLICANT: Baird, Stephen

TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/511,485  
 FILING DATE: 04-AUG-1995  
 CLASSIFICATION: 51A

Search completed: April 16, 2003, 00:58:59  
Job time : 30.6771 secs

[illegible]

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 49.0521 Seconds  
(without alignments)  
3648.005 Million cell updates/sec

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Perfect score: 204  
Sequence: 1 gaagagccagattgaagtc.....ttcccaattgtttttgtt 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues  
Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_5/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_5/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_5/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_5/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_5/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_5/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_5/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_5/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_5/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_5/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_5/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_5/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_5/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_5/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 15: /cgn2\_5/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	204	100.0	2100	9	US-09-201-936-9	Sequence 9, Appli
2	204	100.0	2691	10	US-09-974-592-9	Sequence 9, Appli
3	172	84.3	2540	9	US-09-201-936-3	Sequence 3, Appli
4	172	84.3	5232	10	US-09-974-592-3	Sequence 3, Appli
5	161	78.9	2404	9	US-09-964-899-38	Sequence 38, Appli
6	81.4	39.9	2676	9	US-09-201-936-5	Sequence 5, Appli
7	81.4	39.9	3076	9	US-09-954-531-16	Sequence 16, Appli
8	81.4	39.9	3076	10	US-09-954-556-1635	Sequence 1635, Ap
9	81.4	39.9	6669	10	US-09-974-592-5	Sequence 5, Appli
10	76.8	37.6	240	9	US-09-796-692-3493	Sequence 3493, Ap
11	75.2	36.9	240	9	US-09-796-692-3493	Sequence 6687, Ap
12	72.8	35.7	3151	10	US-09-974-592-13	Sequence 13, Appli
13	71.8	35.2	2291	10	US-09-778-927A-21	Sequence 21, Appli
14	71.8	35.2	2580	9	US-09-201-936-7	Sequence 7, Appli
15	71.8	35.2	3532	10	US-09-880-107-3354	Sequence 3354, Ap
16	71.8	35.2	3732	10	US-09-974-592-7	Sequence 7, Appli
17	71.2	34.9	2416	9	US-09-201-936-41	Sequence 41, Appli
18	63	30.9	2450	9	US-09-201-936-39	Sequence 39, Appli
19	63	30.9	2676	10	US-09-974-592-11	Sequence 11, Appli

20	54.2	26.6	5504	8	US-08-913-322-1	Sequence 1, Appli
21	54.2	26.6	6124	8	US-08-913-322-21	Sequence 21, Appli
22	54.2	26.6	6124	10	US-09-967-768A-184	Sequence 184, Appli
23	54.2	26.6	6133	8	US-08-913-322-2	Sequence 2, Appli
24	54.2	26.6	6228	8	US-08-913-322-23	Sequence 23, Appli
25	51.2	25.1	3773	9	US-10-041-859-1	Sequence 1, Appli
26	35.6	17.5	176373	9	US-10-095-407-17	Sequence 17, Appli
27	34.8	17.1	152331	9	US-10-095-407-16	Sequence 16, Appli
28	33	16.2	616	10	US-09-867-701-1465	Sequence 1465, Ap
29	33	16.2	2880	10	US-09-925-301-415	Sequence 415, App
30	29.2	14.3	592	10	US-09-765-231A-9	Sequence 9, Appli
31	29.2	14.3	30310	10	US-09-800-631-96	Sequence 96, Appli
32	28.6	14.0	1086	10	US-09-815-242-6138	Sequence 6138, Ap
33	28.4	13.9	402	10	US-09-801-574-23	Sequence 23, Appli
34	28.2	13.8	1691139	9	US-10-067-514-1	Sequence 1, Appli
35	28	13.7	1559	10	US-09-867-550-1503	Sequence 1503, Ap
36	28	13.7	1656	9	US-10-038-072-239	Sequence 239, App
37	28	13.7	1656	9	US-10-121-049-239	Sequence 239, App
38	28	13.7	1656	9	US-10-123-904-239	Sequence 239, App
39	28	13.7	1656	9	US-10-140-470-239	Sequence 239, App
40	28	13.7	1656	9	US-10-175-746-239	Sequence 239, App
41	28	13.7	1656	9	US-10-176-918-239	Sequence 239, App
42	28	13.7	1656	9	US-10-137-865-239	Sequence 239, App
43	28	13.7	1656	9	US-10-140-474-239	Sequence 239, App
44	28	13.7	1656	9	US-10-142-431-239	Sequence 239, App
45	28	13.7	1656	9	US-10-142-431-239	Sequence 239, App

## ALIGNMENTS

RESULT 1  
US-09-201-936-9  
; Sequence 9, Application US/09201936  
; Publication No. US20020187946A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; FILE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201,936  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 2100  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-201-936-9

Query Match 100.0%; Score 204; DB 9; Length 2100;  
Best Local Similarity 100.0%; Pred. No. 1.3e-64;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGAGCCAGATTGAAGTCATTTCGAACTGGCCGGACTATGCTCATTTAACCACCCAG 60  
DB 613 GAAGAGCCAGATTGAAGTCATTTCGAACTGGCCGGACTATGCTCATTTAACCACCCAG 672  
QY 61 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120  
DB 673 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 732





Query Match	84.3%	Score 172;	DB 10;	Length 5232;
Best Local Similarity	90.2%	Pred. No. 1e-52;		
Matches 184;	Conservative	0;	Mismatches 20;	Indels 0;
Gaps				0;

Query Match	84.3%	Score 172;	DB 10;	Length 5232;
Best Local Similarity	90.2%;	Pred. No. 1e-52;		
Matches 184;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps
Qy 1	GAAGAAAGCCAGATTGAAGTCATTTCAGAACTGSCCGGACTATGCTCATTTAAACCCOCAGA 60			
Db 520	GAAAGAGCTAGATTAAAGTCCTTCAGAACTGSCCAGACTATGCTCACCTAACCCCAAGA 579			
Qy 61	GAGTTAGCTAGTCTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120			
Db 580	GAGTTAGCAAGTCTGCGACTCTACTACACAGGATTGGTGACCAAGTGCGAGTGTCTTTGT 639			
Qy 121	TGTGGGGGAAACTGAAAATTCGGAAACCTGTGATCGTGCCCTGGTCGAAACACAGGAGA 180			
Db 640	TGTGGTGAAACACTGAAAATTCGGAAACCTGTGATCGTGCCCTGGTCGAAACACAGGCGA 699			
Qy 181	CACTTCCCAATATGCTTTTTTGT 204			
Db 700	CACTTTCCTAATGCTTCTTTGT 723			

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; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

```

Query Match	78.9%	Score 161;	DB 9;	Length 2404;
Best Local Similarity	89.8%	Pred. No. 8.1e-49;		
Matches 184; Conservative	0;	Mismatches 20;	Indels 1;	Gaps
Qy 1	GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGACATATGCTCATTTTAAACCCCCAGA	60		
Db 520	GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGACATATGCTCACCTAACCCCAAGA	579		
Qy 61	GAGTTAGCTAGTGTGCCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT	120		
Db 580	GAGTTAGCAAGTGTGTGACATCTACTACACAGGTTATTTGGTGACCAAGTGCAGTAGCTTTTGT	639		
Qy 121	TGTGGGGGAAACCTGAAAAATTTGGGAACCCCTGTGATCGTGCCTGGTCAG-AAACACGACG	179		
Db 640	TGTGGTGAAACCTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGTAACACAGCG	699		
Qy 180	ACACTTTCCCAATTGCTTTTTTGT	204		
Db 700	ACACTTTCTTAATTGCTTCTTTGT	724		

```

; TITLE OF INVENTION: Process for Identifying
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531

```

```

Query Match          39.98; Score 81.4; DB 9; Length 2676;
Best Local Similarity 66.0%; Pred. No. 1.4e-19;
Matches 134; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY      1  GAAGAAGCCAGATTGAAGTCAATTTACAGAACTGGCCGGACTATGCTCATTTAAACCCCCAGA 60
      11  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      693  GAAATGCCAGATTACTTTACITTTTTCAGACATGGCC---ATTGACITTTTCTGTGCGCAACA 749

QY      61  GAGTTAGTAGTGTGGCCCTACTACACAGGGCTGATGATCAAGTCAGTGCATTCCTTTGT 120
      11  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB      750  GATCTGGCACAGCAGGCGCTTTTACTACATAGAGCCTGGAGACAGAGTGGCTTGCTTTGCC 809

QY      121  TGTGGGGAAACATGAAAAATTTGGAACCCCTGCTGCTCGCTGGCTGTGTCAGAACACAGGAGA 180
      11  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      810  TGTGTGGAATTCAGCAATTTGGAACCGAAGGATATGCTATGTCAGAACACCTGAGA 869

QY      181  CACTTTCCCAATTCGTTTTTTGT 203
      11  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      870  CATTTCCCAAATGCCCATTTAT 892

RESULT 7
US-09-954-531-16
; Sequence 16, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531

```

0.5. NOTSTAY WITHIN FOR /

QY 121 TGTGGGGAAAAC TGA AAAAT TGGGAA



```
FILE REFERENCE: 07891/009004
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/974,592
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 3151
TYPE: DNA
ORGANISM: Mus musculus
US-09-974-592-13

Query Match 35.7%; Score 72.8; DB 10; Length 3151;
Best Local Similarity 61.7%; Pred. No. 2.1e-16;
Matches 116; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 7 GCCAGATTGAAGTCATTTCAGAACTGGCGGACTATGCTCATTTAACCCCGACAGAGTTA 66
DB 1568 GCTCGATTGAGGACATTTCTGTACTGGCCACCTAGTGTCTTCCCTTCAGCCCGAGCAGCTT 1627

QY 67 GCTAGTGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGTGGG 126
DB 1628 GCAAGTGTGGATCTATTACGTGATGCGCAATGATGATGATGATGATGATGATGAT 1687

QY 127 GGAAGAACTGAAATTTGGGAACCTCTGATCGTGGCTGTGATGATGATGATGATGATGAT 186
DB 1688 GTGGCTTGAAGTGTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCAAATGGTTT 1747

QY 187 CCCAATTG 194
DB 1748 CCAAGGTG 1755

RESULT 13
US-09-778-927A-21
Sequence 21, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rafi et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL134453
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 2291
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(2291)
OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-21

Query Match 35.2%; Score 71.8; DB 10; Length 2291;
Best Local Similarity 63.1%; Pred. No. 4.3e-16;
Matches 128; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCGGACTATGCTCATTTAACCCCGCAGA 60
DB 1922 GAAGAAGCCAGATTTCCTTACCTACCATATGTGGCC---ATTAACTTTTGTCCACCATCA 1978

QY 61 GAGTTAGCTAGTGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGT 120
DB 61 GAGTTAGCTAGTGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGT 120
```

```
DB 1979 GAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGCTAGCTGCTTTGCC 2038
QY 121 TGTGGGGGAAACTGAAATAATTTGGGAACCTGTGATCGTCCCTGGTTCAGAACACAGAGA 180
DB 2039 TGTGTCGGGAAGCTCAGTAACCTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGA 2098
QY 181 CACTTTCCCAATTGCTTTTGT 203
DB 2099 CATTTCCTCCAACTGTCCATTTT 2121

RESULT 14
US-09-201-936-7
Sequence 7, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2580
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (2412)...(2412)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match 35.2%; Score 71.8; DB 9; Length 2580;
Best Local Similarity 63.1%; Pred. No. 4.6e-16;
Matches 128; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCGGACTATGCTCATTTAACCCCGCAGA 60
DB 787 GAAGAAGCCAGATTTCCTTACCTACCATATGTGGCC---ATTAACTTTTGTCCACCATCA 843

QY 61 GAGTTAGCTAGTGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGT 120
DB 844 GAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGCTAGCTGCTTTGCC 903

QY 121 TGTGGGGGAAACTGAAATAATTTGGGAACCTGTGATCGTCCCTGGTTCAGAACACAGAGA 180
DB 904 TGTGTCGGGAAGCTCAGTAACCTGGGAACCGAAGGATAATGCTATGTCAGAACACCGGAGG 963

QY 181 CACTTTCCCAATTGCTTTTGT 203
DB 964 CATTTCCTCCAACTGTCCATTTT 986

RESULT 15
US-09-880-107-3354
Sequence 3354, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
```



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds  
(without alignments)  
3384.833 Million cell updates/sec

Title: us-09-654-743-50  
Perfect score: 204  
Sequence: 1 gaagaagccagattgaagtc.....ttcccaattgtttttgtt 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em_estmu.*
5: em_estov.*
6: em_estpl.*
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8: em_estc.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
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22: em_gss_fun.*
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27: em_gss_fod.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	203	99.5	436	9	AI326613 mn83e12.y
2	193.4	94.8	375	9	AA097958 mn83e12.r
3	172	84.3	822	12	BG502660 602549490
4	150.2	73.6	1041	13	BM459898 AGENCOURT
5	144.2	70.7	1020	13	BM554544 AGENCOURT
6	118.2	57.9	1130	13	BM553272 AGENCOURT

7	97.2	47.6	742	13	BI329221
8	81.4	39.9	557	9	AI051610
9	81.4	39.9	886	14	BQ652590
10	79.2	38.8	593	13	BJ096099
11	78.2	38.3	567	13	BI961039
12	78.2	38.3	768	13	BM423292
13	77.2	37.8	459	13	BM446366
14	73.4	36.0	422	10	AW898626
15	72	35.3	298	12	BF016190
16	71.8	35.2	401	12	BF095673
17	71.8	35.2	889	14	BQ720079
18	71.8	35.2	895	14	BQ884287
19	71	34.8	959	13	BM458775
20	70.2	34.4	512	13	BI326908
21	70.2	34.4	611	13	BM536852
22	70.2	34.4	649	10	AW949508
23	69.8	34.2	837	12	BG743309
24	68.8	33.7	851	13	BI253303
25	68.8	33.7	896	14	BQ439248
26	68	33.3	286	9	AA473594
27	67	32.8	681	12	BF611032
28	66	32.4	673	9	AL640649
29	64.8	31.8	590	10	BE268377
30	64.8	31.8	953	17	CNS04211
31	64.4	31.6	936	14	C81977
32	64	31.4	450	12	BG729302
33	64	31.4	595	9	AI558531
34	62.4	30.6	592	13	BJ059822
35	60.2	29.5	441	13	BM312708
36	60.2	29.5	563	9	AA702174
37	60.2	29.5	652	10	AV704923
38	58.2	28.5	354	9	AA354707
39	57	27.9	302	14	R83677
40	57	27.9	780	13	BI771720
41	56.2	27.5	936	13	BM013796
42	55.4	27.2	341	10	AW375598
43	55.4	27.2	354	10	AW375594
44	55.4	27.2	402	10	AW846507
45	55.4	27.2	531	10	AW375599

#### ALIGNMENTS

RESULT 1  
AI326613  
LOCUS  
DEFINITION  
AI326613.1 GI:4061042  
ACCESION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI326613  
mn83e12.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone  
IMAGE:550702 5' similar to SW:IAPIX\_MOUSE Q60989 X-LINKED INHIBITOR  
OF APOPTOSIS PROTEIN ; mRNA sequence.

AI326613  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 436)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Thelning, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMHI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.wustl.edu  
This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:331494  
 This read is a RESEQUENCE of a previously sequenced mouse clone  
 This read has been verified (found to hit its original self in the  
 correct orientation)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 417.  
 Location/Qualifiers  
 1. .436

## FEATURES

source

/organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:50702"  
 /clone\_lib="Stratagene mouse Tcell 937311"  
 /tissue\_type="Tcell"  
 /dev\_stage="M30 CD4+ cells"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: blood; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;  
 Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG  
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' "

BASE COUNT 119 a 92 c 108 g 116 t 1 others  
 ORIGIN

Query Match 99.5%; Score 203; DB 9; Length 436;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-57;  
 Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATCTCATTTAAACCCCGAGA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATCTCATTTAAACCCCGAGA 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGAGA 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGAGA 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 CACTTCCCAATTGCTTTTGT 204  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 CACTTCCCAATTGCTTTTGT 384

## RESULT 2

AA097958

LOCUS

DEFINITION mm89el2.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone  
 IMAGE:50702 5' similar to TR:G1145261 G1145261 MIHA. ;, mRNA  
 sequence.

ACCESSION

AA097958

VERSION

AA097958.1

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 375)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:331494  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28ml3 rev1 Et from Amersham  
 High quality sequence stop: 191.  
 Location/Qualifiers  
 1. .375

## FEATURES

source

/organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:50702"  
 /clone\_lib="Stratagene mouse Tcell 937311"  
 /tissue\_type="Tcell"  
 /dev\_stage="M30 CD4+ cells"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: blood; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;  
 Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG  
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' "

BASE COUNT 109 a 86 c 89 g 91 t  
 ORIGIN

Query Match 94.8%; Score 193.4; DB 9; Length 375;  
 Best Local Similarity 99.5%; Pred. No. 4.4e-54;  
 Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATCTCATTTAAACCCCGAGA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATCTCATTTAAACCCCGAGA 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGAGA 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGAGA 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 CACTTCCCAATTGCTTTTGT 195  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 CACTTCCCAATTGCTTTTGT 375

## RESULT 3

BG502660

LOCUS

DEFINITION 60234949DF1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4657102 5',  
 mRNA sequence.

ACCESSION

BG502660

VERSION

BG502660.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 822)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONETECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCMI449 row: c column: 23  
 High quality sequence stop: 670.  
 Location/Qualifiers  
 1. .822

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4657102"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT      236 a   161 c   201 g   222 t      2 others
ORIGIN

```

```

Query Match      84.3%; Score 172; DB 12; Length 822;
Best Local Similarity 90.2%; Pred. No. 1e-46;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCCAGATTCAAGTCATTTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 60
D 337 GAAGAAGCTAGATAAGTCTTTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 396
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
D 397 GAGTTAGCAAGTGTGGACTCTACTACACAGGATTGTTGACCAAGTGCAGTCTTTGT 456
QY 121 TGTGGGGAAACTGAAAAATTTGGAAACCTGTGATCGTGGCTGTCAGAACACAGGAGA 180
D 457 TGTGCTGAAACTGAAAAATTTGGAAACCTGTGATCGTGGCTGTCAGAACACAGGCGA 516
QY 181 CACTTTCCTCAATGCTTTTGT 204
D 517 CACTTTCCTCAATGCTTTTGT 540

```

```

RESULT 4
BM459898
LOCUS      BM459898      1041 bp      mRNA      linear      EST 05-FEB-2002
DEFINITION AGENCOURT_6422054 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
5', mRNA sequence.
ACCESSION  BM459898
VERSION     BM459898.1 GI:18508938
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1041)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATCC
Email: cgapbs-re@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12215 row: d column: 08
High quality sequence stop: 567.
Location/Qualifiers
1..1041
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

/clone="IMAGE:5532247"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."
BASE COUNT      297 a   208 c   266 g   269 t      1 others
ORIGIN

```

```

Query Match      73.6%; Score 150.2; DB 13; Length 1041;
Best Local Similarity 83.3%; Pred. No. 2.4e-39;
Matches 170; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTCAAGTCATTTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 60
D 553 GAAGAAGCTAGATAAGTCTTTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 612
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
D 613 GAGTTAGCAAGTGTGGACTCTACTACACAGGATTGTTGACAGTGCAGTCTTTGT 672
QY 121 TGTGGGGAAACTGAAAAATTTGGAAACCTGTGATCGTGGCTGTCAGAACACAGGAGA 180
D 673 TGTGCTGAAACTGAAAAATTTGGAAACCTGTGATCGTGGCTGTCAGAACACAGGCGA 732
QY 181 CACTTTCCTCAATGCTTTTGT 204
D 733 CACTTTCCTCAATGCTTTTGT 756

```

```

RESULT 5
BM554544
LOCUS      BM554544      1020 bp      mRNA      linear      EST 20-FEB-2002
DEFINITION AGENCOURT_6545864 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742590
5', mRNA sequence.
ACCESSION  BM554544
VERSION     BM554544.1 GI:18794228
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: p column: 15
High quality sequence stop: 730.
Location/Qualifiers
1..1020
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

REFERENCE
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: p column: 15
High quality sequence stop: 730.
Location/Qualifiers
1..1020
/organism="Homo sapiens"
/db_xref="taxon:9606"

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FEATURES
source
1..1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5742590"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

```



46 CATTTAACCCCCAGAGAGTTAGCTAGTGCCTCTACTACAGGGGC-TGATGATCA 104

Db	279	TGTGGTGGAAATGTGACCAATTGGGACCCAGAGTAATGCTATGTCAGACACCTGAGA	220
QY	181	CACCTTCCCAATGCTTTTTTGT	203
Db	219	CAITTTCCCAATGCCCAATTAT	197
RESULT 9			
BQ652590			
LOCUS			
DEFINITION	BQ652590	886 bp	mrna
	5', mRNA sequence.		linear
ACCESSION	BQ652590		CDNA clone IMAGE:6298025
VERSION	BQ652590.1	GI:21776762	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 886)		
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>		
	Tissue procurement: CGAP (Stanford)		
	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>		
	Plate: L1CM2508 row: g column: 18		
	High quality sequence stop: 638.		
FEATURES			
source	1..886		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6298025"		
	/clone_lib="NIH_MGC_100"		
	/tissue_type="hepatocellular carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:		
	ECORI; CDNA made by oligo-dT priming. Directionally cloned		
	into ECORI/XhoI sites using the following 5' adaptor:		
	GGCAGCAG(G). Size-selected >500bp for average insert size		
	1.8kb. Library constructed by Ling Hong in the laboratory		
	of Gerald M. Rubin (University of California, Berkeley)		
	using ZAP-CDNA synthesis kit (Stratagene) and Superscript		
	II RT (Life Technologies). Note: this is a NIH_MGC		
	Library."		
BASE COUNT	255 a 193 c 186 g 250 t	2	others
ORIGIN			
Query Match	39.94;	Score 81.4;	DB 14;
Best Local Similarity	66.04;	Pred. No. 3.2e-16;	Length 886;
Matches	134;	Conservative 0;	Mismatches 66;
			Indels 3; Gaps 1;
QY	1	GAAAGCCAGATTGAAGTCAATTCATTCAGACATGGCGGACTATGCTCATTTACCCCGAGA	60
Db	239	GAAATGCGAGATTACTTTACTTTTTTCAGACATGGCC---ATTGACTTTTCTGTGCGCAACA	295
QY	61	GAGTTAGTACTGTGGCTCTACTACACAGGGCTGATCAAGTCAATGCTTTTGT	120
Db	296	GATCTGGCAAGCAGGGCTTTTACTTACATAGAGCTGGAGACAGAGTGGCTTGCTTGGC	355
QY	121	TGTGGGGAAACATGAAAAATGGGAACCCCTGTGATCGTGTGTCAGAACACAGGAGA	180
Db	356	TGTGGTGGAAATGTGAGCAATGGGACCGGAGGATATGCTATGTCTCAGACACCTGAGA	415
QY	181	CACCTTCCCAATGCTTTTTTGT	203
Db	416	CATTTCCTCCCAATGCCCAATTAT	438

```

RESULT 10
BJ096099
DEFINITION
  593 bp mRNA linear EST 12-DEC-2001
  Xenopus laevis cDNA clone XL152k19 5', mRNA sequence.
ACCESSION
  BJ096099
VERSION
  BJ096099.1 GI:17596868
KEYWORDS
  EST.
SOURCE
  African clawed frog.
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
  Xenopus laevis
  Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
  Y.
  Expressed genes in X. laevis embryo
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
    1..593
    /organism="Xenopus laevis"
    /db_xref="taxon:8355"
    /clone="XL152k19"
    /clone_lib="NIBB Mochii normalized Xenopus early gastrula
    library"
    /tissue.type="whole embryo"
    /dev.stage="stage 10.5"
    /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
    were oligo-dT primed and directionally cloned. Staging
    according to Nieuwkoop and Faber. Library is subtracted
    and was constructed by N. Garrett and A.M. Zorn,
    (Wellcome/CRC Institute)."
  BASE COUNT
    175 a 129 c 137 g 152 t
  ORIGIN
    Query Match 38.8%; Score 79.2; DB 13; Length 593;
    Best Local Similarity 72.9%; Pred. No. 1.5e-15;
    Matches 102; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
    QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGCTATGCTCATTTAAACCCCGAGA 60
    || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    Db 453 GAGGAAGCCAGACTGCAACATTTCAAAACTGGCCAGGCTATTCGCCGTTAATGCCAAA 512
    QY 61 GAGTTAGCTAGTGGCTGCTCTACTACAGAGGGCTGATGATCAAGTGAATGCTTTTGT 120
    || || || || || || || || || || || || || || || || || || || || ||
    Db 513 GAGCTTGCCAAATGACAGTCTCTTTTATACGATCAACGACGATCAATGCTTTTGT 572
    QY 121 TGTGGGGAAACTGAAAAA 140
    ||||| ||||| || ||
    Db 573 TGTGGTGGAAACTAATGAA 592
  RESULT 11
  BJ096099
  LOCUS
  DEFINITION
    567 bp mRNA linear EST 22-OCT-2001
    MON01_5_C10_b1_A005 Monocytes (MON01) Equus caballus cDNA, mRNA
    sequence.
  ACCESSION
    BJ096099
  VERSION
    BJ096099.1 GI:16319242
  KEYWORDS
    EST.
  SOURCE
    horse.
  ORGANISM
    Equus caballus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
  REFERENCE
    AUTHORS
      Vandenplas, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E.,
      Gingle, A.R., Pratt, L.H. and Moore, J.N.
      An EST database from equine (Equus caballus) monocytes
      Unpublished (2001)
      Contact: Cordonnier-Pratt MM
      Laboratory for Genomics and Bioinformatics
      The University of Georgia, Department of Plant Biology
      Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
      Tel: 706 542 1860
      Fax: 706 583 0210
      Email: mmpratt@cuga.edu
      Sequences have been trimmed to exclude PolyA, vector and regions
      below three prime quality 16. The threshold for high quality sequence is
      20. Three prime sequences, which are obtained with PolyTMix or T7
      sequencing primer, are presented as the reverse complement.
      Seq primer: JEN REV
      High quality sequence stop: 534
      POLYA=No.
  FEATURES
    source
      Location/Qualifiers
        1..567
        /organism="Equus caballus"
        /db_xref="taxon:9796"
        /clone_lib="Monocytes (MON01)"
        /cell_type="Isolated peripheral blood monocytes stimulated
        with E. coli lipopolysaccharide"
        /note="Vector: pBluescript SK(-) from Lambda ZapII;
        Site_1: XhoI; Site_2: EcoRI. The library was made from
        poly-A RNA in the cloning vector lambdaB ZapII. Clones to
        be sequenced were prepared by mass excision."
      BASE COUNT
        147 a 130 c 136 g 154 t
      ORIGIN
        Query Match 38.3%; Score 78.2; DB 13; Length 567;
        Best Local Similarity 65.0%; Pred. No. 3.1e-15;
        Matches 132; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
        QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGCTATGCTCATTTAAACCCCGAGA 60
        || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
        Db 96 GAAAAGCCAGATTAATCTCACTTTCCAGATGTGGCG--CTGACCTTTCTGTGCCCAACA 152
        QY 61 GAGTTAGCTAGTGGCTGCTCTACTACAGAGGGCTGATGATCAAGTGAATGCTTTTGT 120
        || || || || || || || || || || || || || || || || || || || || ||
        Db 153 GATCTGGCAAAAGCTGGCTTTTACTACATAGGACCCGGGACAGAGTGGCTGCTTTGCC 212
        QY 121 TGTGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGA 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
        Db 213 TGTGGTGGAAATTTGAGCAATTTGGGAACCGAGGATGATGCTATGTCGGAACACCTGAGA 272
        QY 181 CACTTTCCTCAATGCTTTTGT 203
        || || ||||| |||||
        Db 273 CATTTCCTCAATGCTTTTGT 295
  RESULT 12
  BJ096099
  LOCUS
  DEFINITION
    PLATE4_F12 Rhesus Macaca mulatta cDNA, mRNA sequence.
  ACCESSION
    BJ096099
  VERSION
    BJ096099.1 GI:18392786
  KEYWORDS
    EST.
  SOURCE
    rhesus monkey.
  ORGANISM
    Macaca mulatta
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
    Cercopithecoinae; Macaca.
  REFERENCE
    AUTHORS
      Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
      Holzman, T.
      Expressed sequence tags from Rhesus macaque spleen
      Unpublished (2002)
      Contact: Holzman T
      Katze lab
  TITLE
    JOURNAL
    COMMENT

```

University of Washington  
Box 358070, Seattle, WA 98195-8070, USA  
Tel: 206 732 6136  
Fax: 206 732 6055  
Email: tedelocke@u.washington.edu  
PLATE4\_F12 768 bases; 37.1 mean phred score.

## FEATURES

Location/Qualifiers  
1..768

/organism="Macaca mulatta"

/db\_xref="taxon:9544"

/clone\_lib="Rhesus"

/tissue\_type="spleen"

/dev\_stage="adult"

/note="vector: pbluescript SK; SIV-associated"

centroblastic non-Hodgkin's lymphoma"

216 a 161 c 174 g 217 t

## BASE COUNT

ORIGIN

Query Match 38.3%; Score 78.2; DB 13; Length 768;

Best Local Similarity 65.0%; Pred. No. 3.6e-15;

Matches 132; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAGCTATTTCAGAACTGGCGGAGTATGCTCATTTTAAACCCACAGA 60

DB 307 GAAAGGCCAGATTACTTTCAGACGTGGCC--ATTGACTTTTCTGTGCGCAACA 363

QY 61 GAGTTAGTCTGCTGGCTCTACTACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120

DB 364 GATCGGCAAAAGCAGGCTTTTACTACCTTGGACCTGGAGACAGAGTGGCTTGTGCC 423

QY 121 TGTGGGGAAACATGAAAATTTGGAACTTGGACCTGTGCTGCTGTCAGACACAGGAGA 180

DB 424 TGTGGCGAAAATTGAGCACTTGGGACCGGAGGATATGCAATGTCAGACACCTGAGA 483

QY 181 CACTTTCCCAATTTGCTTTTGT 203

DB 484 CATTTCCTCAATGCTTTTAT 506

## RESULT 13

BM446366

LOCUS

11L6H6.abl Bos taurus Ileum #1 library Bos taurus cDNA, mRNA EST 05-FEB-2002

DEFINITION

sequence.

ACCESSION

BM446366

VERSION

BM446366.1

KEYWORDS

EST.

SOURCE

COV.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W., Gordon

, P.M.K. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract

Unpublished (2002)

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410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada

Tel: 780 492 0159

Fax: 780 492 0265

Email: smoores@afns.ualberta.ca

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POLYA-No.

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EcoRI; Site:2; Xho I"

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DB 269 GAAAGGCCAGATTACTTACCTTCCAGATGTGGCG--TTGACTTTTCTGTCCACACA 325

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DB 326 GACCTGGCAAAAGCAGGCTTTTATTACATAGGACCTGGAGATAGATGGCTTGTGCC 385

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DB 386 TGTGTGGAAACATTGAGCAATTGGGACCGGAGGATGCTTATGTCAGAACACCTGAGA 445

QY 181 CACTTTCCCAATTG 194

DB 446 CATTTCCTCAATGCTTTTAT 459

## RESULT 14

AW898626/c

LOCUS

RC1-NN0073-090500-012-e06 NN0073 Homo sapiens cDNA, mRNA sequence.

ACCESSION

AW898626

VERSION

AW898626.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Pais, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=62-RCL-NN0073-090

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/dev\_stage="Adult"

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 698.026 Seconds  
(without alignments)  
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Perfect score: 138  
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
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- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
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- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

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1	138	100.0	1659	6	E31042	E31042 Method for
2	138	100.0	1659	9	BC032974	U32974 Human IAP-1
3	138	100.0	2086	9	BC032729	BC032729 Homo sapi
4	138	100.0	2404	6	AX429575	AX429575 Sequence
5	138	100.0	2540	6	AR103281	AR103281 Sequence
6	138	100.0	2540	6	AX412118	AX412118 Sequence
7	138	100.0	2540	6	HSU45880	U45880 Human X-11a
8	138	100.0	3000	6	AX412131	AX412131 Sequence
9	138	100.0	5232	6	AR106397	AR106397 Sequence
10	138	100.0	5232	6	AR116899	AR116899 Sequence
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c 12	138	100.0	133391	9	HSJ315G1	AL121601 Human DNA
c 13	138	100.0	201197	2	HS424J12	Z82207 Homo sapien
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15	130	94.2	1988	10	MMU36842	U36842 Mus musculu
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17	128.4	93.0	2032	10	AF304333	AF304333 Rattus no
18	128.4	93.0	2468	10	AB033366	AB033366 Rattus no
19	128.4	93.0	3032	10	AF304334	AF304334 Rattus no
c 20	128.4	93.0	185771	2	AC111718	AC111718 Rattus no
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24	125.2	90.7	2691	10	MMU88990	U88990 Mus musculu
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26	122.6	88.8	351	6	AX104958	AX104958 Sequence
27	121	87.7	351	6	AX104964	AX104964 Sequence
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33	117.2	84.9	711	6	AR123871	AR123871 Sequence
34	117.2	84.9	1758	6	AX370787	AX370787 Sequence
35	117.2	84.9	1758	6	AX370789	AX370789 Sequence
36	117.2	84.9	2032	9	AF420440	AF420440 Homo sapi
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45	114	82.6	711	9	AY030053	AY030053 Gorilla g

ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

E31042  
Method for screening substance inhibiting binding to XIAP.  
E31042  
E31042.1 GI:13017307  
JP 1999326328-A/2.  
unidentified.  
unidentified.  
unclassified.  
1 (bases 1 to 1659)  
Kunihiko M.  
Method for screening substance inhibiting binding to XIAP  
Patent: JP 1999326328-A 2 26-NOV-1999;  
KUNIHICO MATSUMOTO

E31042  
1659 bp  
DNA  
linear  
PAT 18-JUN-2001

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COMMENT OS Unidentified
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PD 26-NOV-1999
PF 13-MAY-1998 JP 1998130378
PR KUNIHRO MATSUMOTO
PI
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PC A61K39/395,
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PC A61K33/536,
PC G01N33/536,G01N33/536//C12N15/09,C12P21/08,A61K37/02,
PC A61K37/02, PC A61K37/02,
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FH Key Location/Qualifiers
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QY 121 GACAAGTGTCCTCATGTGC 138
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LOCUS
DEFINITION Human IAP-like protein ILP mRNA, complete cds.
ACCESSION U32974
VERSION U32974.1 GI:1016687
KEYWORDS apoptosis; ring finger; zinc finger.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1659)
Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
Gilfillan,M.C., Shields,H., Hardwick,J.M. and Thompson,C.B.
A conserved family of cellular genes related to the baculovirus iap
gene and encoding apoptosis inhibitors
EMBO J. 15 (11), 2685-2694 (1996)
6256286
PUBMED 8654366
REFERENCE 2 (bases 1 to 1659)
Duckett,C.S. and Thompson,C.B.
Direct Submission
Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
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DB 1456 GCTATCGTTTTTCTTCTTGTGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 1515
QY 121 GACAAGTGTCCTCATGTGC 138
DB 1516 GACAAGTGTCCTCATGTGC 1533
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BC032729 2086 bp mRNA linear PRI 27-JUN-2002
LOCUS
DEFINITION Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369
IMAGE:5532247, mRNA, complete cds.
ACCESSION BC032729
VERSION BC032729.1 GI:21619763
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2086)
Strausberg,R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov

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AKhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,  
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,  
Dierich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,  
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,  
Maduro,O.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,  
Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.

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This clone was selected for full length sequencing because it  
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DEFINITION Sequence 38 from Patent WO026820.  
ACCESSION AX429575  
VERSION AX429575.1 GI:21540833  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,  
Reinhardt,M.W. and Zusan,S.  
TITLE Transgenic drosophila melanogaster expressing beta amyloid

JOURNAL Patent: WO 026820-A 38 04-APR-2002;  
NOVARTIS ERIND VERWALT GMBH (AT)

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QY 121 GACAAGTGCCCATGTGC 138  
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RESULT 5  
ARI03281  
LOCUS 2540 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 1 from patent US 6087173.  
ACCESSION ARI03281  
VERSION ARI03281.1 GI:12814869  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2540)  
AUTHORS Bennett,C.Frank, Ackermann,E.J. and Cowser,L.M.1  
TITLE Antisense modulation of X-linked inhibitor of apoptosis expression  
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
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ACCESSION AX412118  
VERSION AX412118.1 GI:21444581  
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SOURCE human.  
ORGANISM Homo sapiens  
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LOCUS AR106397 5232 bp DNA linear PAT 14-FEB-2001  
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ACCESSION AR106397  
VERSION AR106397.1 GI:12820927  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL Patent: US 6107041-A 3 22-AUG-2000;  
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QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGGCAAAATCTGTATGGATAGAAATATT 60  
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Db 1348 GACCACCTAAGGCGCTGCAAGAGGAGAGCTTTGGCAAAATCTGTATGGATAGAAATATT 1407  
QY 61 GCTATCGTTTTGTTCTGTTGGACATCTAGTCACCTGTGTAACAATGCTGTGAGCAGTT 120  
|||||  
Db 1408 GCTATCGTTTTGTTCTGTTGGACATCTAGTCACCTGTGTAACAATGCTGTGAGCAGTT 1467  
QY 121 GACAAGTGCCCATGTGC 138  
|||||  
Db 1468 GACAAGTGCCCATGTGC 1485  
|||||  
RESULT 10  
LOCUS AR116699 5232 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6133437.  
ACCESSION AR116699  
VERSION AR116699.1 GI:14097021  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;  
FEATURES Location/Qualifiers  
source  
1..5232  
/organism="unknown"  
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others  
ORIGIN  
Query Match 100.0%; Score 138; DB 6; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 2.3e-30;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGGCAAAATCTGTATGGATAGAAATATT 60  
|||||  
Db 1348 GACCACCTAAGGCGCTGCAAGAGGAGAGCTTTGGCAAAATCTGTATGGATAGAAATATT 1407  
QY 61 GCTATCGTTTTGTTCTGTTGGACATCTAGTCACCTGTGTAACAATGCTGTGAGCAGTT 120  
|||||  
Db 1408 GCTATCGTTTTGTTCTGTTGGACATCTAGTCACCTGTGTAACAATGCTGTGAGCAGTT 1467  
QY 121 GACAAGTGCCCATGTGC 138  
|||||  
Db 1468 GACAAGTGCCCATGTGC 1485  
|||||  
Db 1408 GCTATCGTTTTGTTCTGTTGGACATCTAGTCACCTGTGTAACAATGCTGTGAGCAGTT 1467  
QY 121 GACAAGTGCCCATGTGC 138  
Db 1468 GACAAGTGCCCATGTGC 1485  
RESULT 11  
LOCUS HS167P19/c  
DEFINITION Homo sapiens chromosome X clone RP1-167P19 map q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 10 unordered pieces.  
ACCESSION 293014  
VERSION 293014.2 GI:10045109  
KEYWORDS HTGS\_PHASE1; HTGS\_CANCELLED.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 122742)  
AUTHORS Grafham,D.  
TITLE Direct Submission.  
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk  
COMMENT On Sep 9, 2000 this sequence version replaced gi:6981883.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: dj167P19  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: M13; M7815; 18% of reads  
Sequencing vector: plasmid; L08752; 81% of reads  
Chemistry: Dye-terminator ABI; 100% of reads  
Consensus quality: 118637 bases at least Q40  
Consensus quality: 119897 bases at least Q30  
Consensus quality: 120866 bases at least Q20  
Insert size: 121842; sum-of-contigs  
Quality coverage: 6.65x in Q20 bases; sum-of-contigs  
\* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved  
1 18344: contig of 18344 bp in length  
18345 18444: gap of 100 bp  
18445 24822: contig of 6378 bp in length  
24823 24922: gap of 100 bp  
24923 26984: contig of 2062 bp in length  
26985 27084: gap of 100 bp  
27085 36741: contig of 9657 bp in length  
36742 36841: gap of 100 bp  
36842 40798: contig of 3957 bp in length  
40799 40898: gap of 100 bp  
40899 50764: contig of 9866 bp in length  
50765 50864: gap of 100 bp  
50865 60908: contig of 10044 bp in length  
60909 61008: gap of 100 bp  
61009 90700: contig of 29692 bp in length  
90701 90800: gap of 100 bp  
90801 101526: contig of 10726 bp in length  
101527 101626: gap of 100 bp  
101627 122742: contig of 21116 bp in length  
Location/Qualifiers  
FEATURES

```

source
1. .122742
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="q25"
/clone="RPI-167P19"
/clone_lib="RPCI-1"
1. .18344
/note="assembly_fragment:00897
fragment_chain:1"
1845. .24822
/note="assembly_fragment:03100
fragment_chain:1"
24923. .26984
/note="assembly_fragment:01003
fragment_chain:2"
27085. .36741
/note="assembly_fragment:01036
fragment_chain:2"
36842. .40798
/note="assembly_fragment:02480
fragment_chain:3"
40899. .50764
/note="assembly_fragment:02098
fragment_chain:3"
50865. .60908
/note="assembly_fragment:00356"
61009. .90700
/note="assembly_fragment:00910"
90801. .101526
/note="assembly_fragment:02458"
101627. .122742
/note="assembly_fragment:02641"
BASE COUNT 34749 a 24137 c 25101 g 37853 t 902 others
ORIGIN

Query Match 100.0%; Score 138; DB 2; Length 122742;
Best Local Similarity 100.0%; Pred. No. 2e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACAGCTRAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 88514 GACAGCTRAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 88455
|||||

QY 61 GCATCTCTTTTGTCTTCTGTCGACATCTAGTCTGTAACAAATGCTGTAAGCAGTT 120
|||||
Db 88454 GCATCTCTTTTGTCTTCTGTCGACATCTAGTCTGTAACAAATGCTGTAAGCAGTT 88395
|||||

QY 121 GACAAGTGTCCCATGTGC 138
|||||
Db 88394 GACAAGTGTCCCATGTGC 88377

RESULT 12
HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000
LOCUS
DEFINITION
Human DNA sequence from clone RPI-315G1 on chromosome Xq24-25.
Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene
for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene.
ESTs, STSS, GSSs and a putative cpG island, complete sequence.
AL121601
HSDJ315G1.13 GI:7159760
FEATURES
FTG: API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 133391)
AUTHORS
Grafham D.
TITLE
Direct Submission
JOURNAL
Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT
On Mar 6, 2000 this sequence version replaced gi:6983378.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/Celegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RPI-315G1 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RPI-315G1 The true
right end of clone RP6-30A23 is at 100 in this sequence.

FEATURES
source
1. .133391
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="q24-25"
/clone="RPI-315G1"
/clone_lib="RPCI-1"
complement(3738. .4224)
/note="match: GSS: Em:AQ885645"
misc_feature
complement(4112. .4623)
/note="match: GSS: Em:AQ623859"
misc_feature
4617. .5326
/note="match: GSS: Em:AQ740042"
misc_feature
4624. .4824
/note="match: GSS: Em:AQ587673"
misc_feature
4828. .5111
/note="match: GSS: Em:AQ587673"
gene
complement(6712. .7417)
/feature="dJ315G1.1"
CDS
complement(6712. .7417)
/feature="dJ315G1.1"
pseudogene
match: ESTs: Em:AW369746
match: proteins: Tr:Q91510 Tr:O14911 Tr:Q92101 Tr:O18129
Tr:O97111"
/pseudo
/codon_start=1
/evidence=not_experimental
gene
13544. .36179
/feature="API3"
mRNA
join(13544. .14661,16741. .16840,19360. .19438,20853. .20895,
28615. .28815,35110. .36179)
/feature="API3"
/product="dJ315G1.2 (apoptosis inhibitor 3 (XIAP, HILP))"
/note="match: cDNAs: Em:AB033366 Em:U88990 Em:U32574
Em:U45880 Em:U36842
match: ESTs: Em:HSCZQG051 Em:A1628066 Em:AA295472
Em:A1598959 Em:A1418337 Em:A1277821 Em:HSCZQG052
Em:AA987840"
/evidence=not_experimental
CDS
join(13785. .14661,16741. .16840,19360. .19438,20853. .20895,
28615. .28815,35110. .35303)
/feature="API3"

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/note="match: proteins: Tr:O57319 Sw:P98170 Sw:Q90660
Sw:Q13490 Sw:Q60989 Sw:Q62210"
/codon_start-1
/evidence-not_experimental
/product="d3j15g1.2 (apoptosis inhibitor 3 (XIAP, HILP))"
/protein_id="CAB95312.1"
/db_xref="GI:8744934"
/translacion="MTFNSPEGSKTCVPADINKEEVEEFNRLKTRANFPSPGSPVSA
STLARGFLTGEDTVRCRCHAAVDKQSAVGRHRYKSPNCRFINFGFIYENPAM
TQSTNGSQYQYVINYLGSRHFDALPSETHADYLLRTGOVVDISDTIYPRNPAM
YSEEARLKSFQWFDYAHLTRELASAGLYTGIDQVQCCKGKLNKWPEDRAWNS
EHRHFPCFVLGNLIRSEDAVSDRNFPSTNLPNPSMADYEARTFTGTWI
YVSKQELARAGFALGEGDKVCFHCGSGLTDMKPSDPWQHAQWPGCKVYLLEOK
GOEVINIHLSLECLVTRTEKPSLTRIDDTIFQNPWQEAIRMGFSFKDIKI
MEEKIQISKLVLEVLADLVNAQKSMODESSQTSLOKEISTEQLRLQLEKLC
KICMDRIAVFVPCGHLVCKQCAEAVDKPCMYTIVTFKQIFMS"
repeat_region
16117..16170
/note="27 copies 2 mer aa 72% conserved"
complement(join(16759..16840,19360..19438,20853..20895,
28618..28815))
/note="match: GSS: Em:AQ011995"
27268..27447
/note="90 copies 2 mer ta 73% conserved"
complement(28616..28815)
/note="match: GSS: Em:AQ0697308"
complement(29161..29662)
/note="match: GSS: Em:AQ0719253"
29663..29811
/gene="API3"
/note="match: STS: Em:L24583"
31721..31780
/note="30 copies 2 mer tt 73% conserved"
complement(35122..35394)
/note="match: STS: Em:L24579"
35386..35721
/gene="API3"
/note="match: GSS: Em:AQ141934"
38208..38451
/note="match: STS: Em:G42563"
complement(40019..40354)
/note="match: STS: Em:AAQ17266"
complement(40058..40218)
/note="match: STS: Em:G20782"
40354..40395
/note="21 copies 2 mer aa 76% conserved"
complement(41638..42044)
/note="match: GSS: Em:AQ215516"
complement(41858..42269)
/note="match: GSS: Em:AQ191969"
45461..45573
/note="match: STS: Em:L47219"
45462..45573
/note="match: STS: Em:L77256"
55942..56315
/note="match: STS: Em:L40935"
56488..56535
/note="24 copies 2 mer at 77% conserved"
63199..63252
/note="27 copies 2 mer tc 87% conserved"
64782..65078
/note="match: STS: Em:AL031561"
join(69559..69636,70004..70181)
/note="match: GSS: Em:AQ485834 Em:AQ540857"
join(69586..69636,70004..70193)
complement(69632..69815)
/note="match: GSS: Em:AQ223233"
complement(69632..69793)
/note="match: GSS: Em:AQ380019"
complement(69645..69791)
/note="match: GSS: Em:AQ405293"
69653..69814
/note="match: GSS: Em:AQ383553"

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/note="match: STS: Em:B75787"
misc_feature
complement(69661..69771)
/note="match: GSS: Em:AQ394235"
misc_feature
69855..69792
/note="match: GSS: Em:AQ347249"
misc_feature
complement(69921..70100)
/note="match: GSS: Em:AQ323717"
misc_feature
complement(69956..70137)
/note="match: GSS: Em:AQ802964"
69958..70287
/note="match: STS: Em:G42844"
69958..70201
/note="match: GSS: Em:AQ166728"
69958..70109
/note="match: GSS: Em:AQ479649"
misc_feature
complement(69964..70254)
/note="match: GSS: Em:AQ746057"
misc_feature
complement(69964..70177)
/note="match: GSS: Em:AQ390824"
70315..70835
/note="match: GSS: Em:AQ523288"
70643..70747
/note="match: STS: Em:J03078"
70749..70962
/note="match: STS: Em:J03078"
74945..75008
/note="32 copies 2 mer tt 71% conserved"
complement(76754..76989)
/note="match: STS: Em:G04044"
complement(81909..82264)
/note="match: GSS: Em:AQ200989"
81959..82266
/note="match: STS: Em:L41185"
83301..83356
/note="28 copies 2 mer aa 73% conserved"
Query Match
100.0%; Score 138; DB 9; Length 133391;
Best Local Similarity 100.0%; Pred No. 2e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTTGGCAATCTGTATGATAGAAATATT 60
|||||
Db 35124 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTTGGCAATCTGTATGATAGAAATATT 35183
QY 61 GCTATCGTTTTTCTTCTTCTGACATCTAGTACATCTGTAAACAATGCTGCTGAAGCAGTT 120
|||||
Db 35184 GCTATCGTTTTTCTTCTTCTGACATCTAGTACATCTGTAAACAATGCTGCTGAAGCAGTT 35243
QY 121 GACAAGTGTCCTCATGTGC 138
|||||
Db 35244 GACAAGTGTCCTCATGTGC 35261
RESULT 13
HS424J12/c
LOCUS
DEFINITION
Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
ACCESSION
282207
VERSION
282207.3 GI:12331276
KEYWORDS
HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 201197)
AUTHORS
Grafham D.
TITLE
Direct Submission
JOURNAL
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
On Jan 22, 2001 this sequence version replaced gi:10045116.

```

```

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: DJ24J12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 74% of reads
Chemistry: Dye-terminator Big Dye; 25% of reads
Chemistry: Dye-terminator ABI; 96% of reads
Chemistry: Dye-primer-amerham; 2% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 194333 bases at least Q40
Consensus quality: 196512 bases at least Q30
Consensus quality: 198047 bases at least Q20
Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4154: contig of 4154 bp in length
* 4155 4254: gap of 100 bp
* 4255 18703: contig of 14449 bp in length
* 18704 18803: gap of 100 bp
* 18804 20941: contig of 2138 bp in length
* 20942 21041: gap of 100 bp
* 21042 34907: contig of 13866 bp in length
* 34908 35012: gap of 105 bp
* 35013 37508: contig of 2496 bp in length
* 37509 37608: gap of 100 bp
* 37609 52739: contig of 15131 bp in length
* 52740 52839: gap of 100 bp
* 52840 56933: contig of 4094 bp in length
* 56934 57033: gap of 100 bp
* 57034 88245: contig of 31212 bp in length
* 88246 88346: gap of 101 bp
* 88347 93386: contig of 5040 bp in length
* 93387 93486: gap of 100 bp
* 93487 123956: contig of 30470 bp in length
* 123957 124056: gap of 100 bp
* 124057 147917: contig of 23861 bp in length
* 147918 148017: gap of 100 bp
* 148018 176236: contig of 28219 bp in length
* 176237 176336: gap of 100 bp
* 176337 187128: contig of 10792 bp in length
* 187129 187228: gap of 100 bp
* 187229 190824: contig of 3596 bp in length
* 190825 190959: gap of 135 bp
* 190960 201197: contig of 10238 bp in length.
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FEATURES
source
Location/Qualifiers
1. .201197
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP3-424J12"
/clone_lib="RPCI-3"
1. .4154
/note="assembly_fragment:02486
fragment_chain:1"
4255. .18703
/note="assembly_fragment:04764
fragment_chain:1"
18804. .20941
/note="assembly_fragment:03282

```

```

misc_feature
21042. .34907
/note="assembly_fragment:03624
fragment_chain:2"
35008. .37508
/note="assembly_fragment:00340"
37609. .52739
/note="assembly_fragment:00671.0"
52840. .56933
/note="assembly_fragment:01287.0"
57034. .88245
/note="assembly_fragment:01294"
88346. .93386
/note="assembly_fragment:01608"
93487. .123956
/note="assembly_fragment:03234"
124057. .147917
/note="assembly_fragment:04074"
148018. .176236
/note="assembly_fragment:04816"
176337. .187128
/note="assembly_fragment:05488"
187229. .190824
/note="assembly_fragment:05572.0"
190925. .201197
/note="assembly_fragment:03867
clone_end:T7
vector_side:right"
BASE COUNT 55207 a 43266 c 43712 g 57504 t 1508 others >
ORIGIN
Query Match 100.0%; Score 138; DB 2; Length 201197;
Best Local Similarity 100.0%; Pred. No. 1.9e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 154162 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTTGCAAAATCTGTATGGATAGAAATATT 154103
QY 61 GCTATCGTTTTTGTCTCTGTCGACATCTAGTCACATGTTAAACAATCTGCTGAAGCAGTT 120
|||||
Db 154102 GCTATCGTTTTTGTCTCTGTCGACATCTAGTCACATGTTAAACAATCTGCTGAAGCAGTT 154043
QY 121 GACAAGTGTCCCATGTGC 138
|||||
Db 154042 GACAAGTGTCCCATGTGC 154025
RESULT 14
AL390123
LOCUS
DEFINITION
Human DNA sequence from clone RP11-566F5 on chromosome 10, complete
sequence.
ACCESSION AL390123
VERSION AL390123.14 GI:16304934
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 158093)
AUTHORS Laird,G.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
COMMENT On Oct 21, 2001 this sequence version replaced gi:15020926.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

```

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10> RP11-566F5 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-566F5. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-271113 is at 156094 in this sequence. The true right end of clone RP11-402N18 is at 2000 in this sequence.

## FEATURES

## source

Location/Qualifiers  
 1. .158093  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-566F5"  
 /clone\_lib="RP11-11.2"  
 BASE COUNT 49096 a 31903 c 31075 g 46019 t  
 ORIGIN

Query Match 95.4%; Score 131.6; DB 9; Length 158093;  
 Best Local Similarity 97.1%; Pred. No. 1.5e-28;  
 Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGGCGCTGCAAGAGGAGAGCTTTGGCAAAATCTGTAGATAGAAATATT 60  
 |||||  
 Db 89067 GAGCAGCTAAGGCACTGCAAGTGGAGAGCTTTGGCAAAATCTGTAGATAGAAATATT 89126  
 |||||

QY 61 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACTGTAAACAATGTGCTGAAGCAGTT 120  
 |||||  
 Db 89127 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACTGTAAACAATGTGCTGAAGCAGTT 89186  
 |||||

QY 121 GACAAGTGCCCATGTGC 138  
 |||||  
 Db 89187 GACAAGTGCCCATGTGC 89204  
 |||||

## RESULT 15

MMU36842 1988 bp mRNA linear ROD 05-JUN-1996  
 LOCUS Mus musculus IAP homolog A (MIHA) mRNA, complete cds.  
 DEFINITION U36842  
 ACCESSION U36842  
 VERSION U36842.1 GI:1145260

## KEYWORDS

SOURCE house mouse strain-C57 Black 6 x CBA.

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 1988)

## REFERENCE

Uren,A.G., Pakusch,M., Hawkins,C.J., Puls,K.L. and Vaux,D.L.  
 Cloning and expression of apoptosis inhibitory protein homologs  
 that function to inhibit apoptosis and/or bind tumor necrosis  
 factor receptor-associated factors  
 Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)

## JOURNAL

MEDLINE 96209843

## PUBMED

8643514  
 2 (bases 1 to 1988)

AUTHORS Vaux,D.L., Uren,A.G. and Pakusch,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall  
 Institute, Royal Parade, Parkville, Victoria 3050, Australia

## FEATURES

## source

Location/Qualifiers  
 1. .1988  
 /organism="Mus musculus"  
 /strain="C57 Black 6 x CBA"  
 /db\_xref="taxon:10090"  
 /sex="female"  
 /tissue\_type="liver"  
 /dev\_stage="6-8 weeks old"  
 1. .1988  
 /gene="MIHA"  
 212. 1702  
 /gene="MIHA"  
 /note="apoptosis inhibitor; homolog of Baculovirus IAP  
 protein"

## gene

## CDS

misc\_feature 287..490  
 /gene="MIHA"  
 /note="BIR repeat 1"  
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 /gene="MIHA"  
 /note="BIR repeat 2"  
 misc\_feature 1001..1198  
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 /note="BIR repeat 3"  
 misc\_feature 1556..1650  
 /gene="MIHA"  
 /note="RING finger"

BASE COUNT 605 a 367 c 459 g 557 t

## ORIGIN

Query Match 94.2%; Score 130; DB 10; Length 1988;  
 Best Local Similarity 96.4%; Pred. No. 5.6e-28;  
 Matches 133; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGGCGCTGCAAGAGGAGAGCTTTGGCAAAATCTGTATGGATAGAAATATT 60  
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 Db 1523 GAGCAGCTAAGGGCGCTTACAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1582  
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QY 61 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACTGTAAACAATGTGCTGAAGCAGTT 120  
 |||||

Db 1583 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACTGTAAACAATGTGCTGAAGCAGTT 1642  
 |||||

QY 121 GACAAGTGCCCATGTGC 138  
 |||||

Db 1643 GACAAGTGCCCATGTGC 1660  
 |||||

Search completed: April 15, 2003, 23:25:21  
 Job time : 765.026 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 92.2396 seconds  
(without alignments)  
3369.223 Million cell updates/sec

Title: US-09-654-743-48  
Perfect score: 138  
Sequence: 1 gagcagctaaagccctgca.....ttgacaagtgtcccatgtgc 138

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
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13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	138	100.0	489	22	ABAA3584
C 2	138	100.0	489	22	AA112335
C 3	138	100.0	489	22	AA102249
C 4	138	100.0	1533	23	AA574582
C 5	138	100.0	1533	23	AA588274
C 6	138	100.0	1659	21	AAZ48862
C 7	138	100.0	2404	24	AAK99405
C 8	138	100.0	2540	18	AAAT70836
C 9	138	100.0	2540	21	AAA64901
					Human breast cell
					Probe #2268 for ge
					Probe #2240 used t
					DNA encoding novel
					DNA encoding novel
					Human XIAP coding
					DNA of APP related
					Human apoptosis in
					Human X-linked inh

10	138	100.0	2540	24	ABK93869	Human cDNA encodin
11	138	100.0	3000	24	ABK93875	Human cDNA encodin
12	138	100.0	5232	19	AAV55038	Human XIAP coding
13	134	97.1	148	22	ABA48694	Human breast cell
C 14	134	97.1	148	22	AA121530	Probe #11463 for g
C 15	134	97.1	148	22	AA107226	Probe #7217 used t
16	130	94.2	1988	18	AAAT72710	Mouse inhibitor of
17	125.2	90.7	2100	18	AAAT70839	Mouse apoptosis in
18	125.2	90.7	2100	24	ABK93872	Mouse cDNA encodin
19	125.2	90.7	2691	19	AAV55041	Murine XIAP coding
20	124.2	90.0	351	22	AAAD03580	Rhesus IAP-like pr
21	122.6	88.8	351	22	AAAD03576	Baboon IAP-like pr
22	121	87.7	351	22	AAAD03579	Gorilla IAP-like p
23	119.4	86.5	802	20	AAK03018	Human IL-1ra BAC c
24	119.4	86.5	1752	22	AAAD03575	Human IAP-like pro
C 25	119.4	86.5	2211	20	AAK02975	Human IL-1ra BAC c
26	117.8	85.4	351	22	AAAD03577	Chimpanzee IAP-lik
27	117.2	84.9	711	21	AAA06940	DNA encoding human
28	117.2	84.9	1559	24	ABK13197	Human testes speci
29	117.2	84.9	1758	24	ABK14677	Human inhibitor of
30	117.2	84.9	1758	24	ABK14678	Human inhibitor of
31	117.2	84.9	4993	22	AAAD03581	Human IAP-like pro
32	114	82.6	711	22	AAAD03582	Chimpanzee IAP-lik
33	114	82.6	711	22	AAAD03583	Gorilla IAP-like p
34	108.2	78.4	348	22	AAAD03578	Cynomolgus IAP-lik
35	61.2	44.3	2416	18	AAAT70841	Mouse apoptosis in
36	61.2	44.3	2416	24	ABK93874	Mouse cDNA encodin
37	61.2	44.3	2862	18	AAAT61592	Murine c-IAP. Mus
38	61.2	44.3	3151	19	AAV55043	Murine XIAP-2 codi
39	60.2	43.6	2474	18	AAAT70840	Mouse apoptosis in
40	60.2	43.6	2474	24	ABK93873	Mouse cDNA encodin
41	58.6	42.5	2601	18	AAAT61591	Human c-IAP2. Hom
42	58.6	42.5	2676	19	AAV55042	Murine XIAP-1 codi
43	58.6	42.5	3076	18	AAAT72712	Human inhibitor of
44	58.6	42.5	3076	20	AAZ41005	Human cellular inh
45	58.6	42.5	3076	20	AAZ22096	Human cellular inh

## ALIGNMENTS

RESULT 1  
ABAA3584/C  
ID ABAA3584 standard; DNA; 489 BP.  
XX AC ABAA3584;  
XX AC  
XX AC  
XX 01-FEB-2002 (first entry)  
XX DE Human breast cell single exon nucleic acid probe #2279.  
XX DE Human breast cell single exon nucleic acid probe #2279.  
XX KW Human; microarray; single exon probe; gene expression; breast;  
XX KW disease; cancer; ss.  
XX OS Homo sapiens.  
XX OS  
XX PN WC200157271-A2.  
XX XX  
XX PD 09-AUG-2001.  
XX XX  
XX PF 30-JAN-2001; 2001WO-US00662.  
XX XX  
XX PR 04-FEB-2000; 2000US-0180312.  
XX PR 26-MAY-2000; 2000US-0207456.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-0234587.  
XX PR 27-SEP-2000; 2000US-0236359.  
XX PR 04-OCT-2000; 2000US-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX PI





PA (MOLE-) MOLECULAR DYNAMICS INC.  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-476286/51.  
XX  
XX Novel single exon nucleic acid probe used to measuring gene expression  
PT in a human breast -  
PT  
XX  
XX Claim 25; SEQ ID No 2240; 322pp; English.  
PS  
XX The present invention relates to novel single exon nucleic acid probes.  
XX The present sequence is one such probe. The probes are useful for  
CC measuring human gene expression in a human breast sample, where the probe  
CC hybridises at high stringency to a nucleic acid expressed in the human  
CC breast. The probes are useful for predicting, diagnosing, grading,  
CC staging, monitoring and prognosing diseases of the human breast,  
CC particularly those diseases with polygenic aetiology. The diseases  
CC include: breast cancer, disorders of development, inflammatory diseases  
CC of the breast, fibrocystic changes, proliferative breast disease and  
CC non-carcinoma tumours.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 489 BP; 175 A; 90 C; 73 G; 151 T; 0 other;  
Query Match 100.0%; Score 138; DB 22; Length 489;  
Best Local Similarity 100.0%; Pred. No. 9.4e-34;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 60  
Db 450 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 391  
Qy 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 120  
Db 390 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 331  
Qy 121 GACAAGTGTCCTCATGTGC 138  
Db 330 GACAAGTGTCCTCATGTGC 313  
RESULT 4  
AAS74582  
ID AAS74582 standard; cDNA; 1533 BP.  
XX  
XX AAS74582;  
AC  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #10386.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR

DR P-PSDB; ABG10395.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
XX Claim 1; SEQ ID No 10386; 103pp; English.  
PS  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1533 BP; 362 A; 421 C; 392 G; 358 T; 0 other;  
Query Match 100.0%; Score 138; DB 23; Length 1533;  
Best Local Similarity 100.0%; Pred. No. 1.3e-33;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 60  
Db 1354 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 1413  
Qy 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 120  
Db 1414 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 1473  
Qy 121 GACAAGTGTCCTCATGTGC 138  
Db 1474 GACAAGTGTCCTCATGTGC 1491  
RESULT 5  
AAS88274  
ID AAS88274 standard; cDNA; 1533 BP.  
XX  
XX AAS88274;  
AC  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #24078.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
DR

XX (HYSE-) HYSEQ INC.  
PA Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX P-PSDB; ABG24087.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity  
XX Claim 1; SEQ ID No 24078; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. AAS64197-AAS94564 represent novel human  
XX diagnostic coding sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 1533 BP; 362 A; 421 C; 392 G; 358 T; 0 other;  
Query Match 100.0%; Score 138; DB 23; Length 1533;  
Best Local Similarity 100.0%; Pred. No. 1.3e-33;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 60  
DB 1354 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 1413  
QY 61 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120  
DB 1414 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1473  
QY 121 GACAAGTGTCCCATGTGC 138  
DB 1474 GACAAGTGTCCCATGTGC 1491  
RESULT 6  
AAZ48862  
ID AAZ48862 standard; cDNA; 1659 BP.  
XX AC AAZ48862;  
XX DT 24-MAR-2000 (first entry)  
XX DE Human XIAP coding sequence.  
XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;  
XX transforming growth factor-beta activated kinase 1; monocyte migration;  
XX TAK1 binding protein 1; extracellular matrix protein production;  
XX cell growth inhibitor; beta-amyloid protein deposition;  
XX immunosuppression; Transforming growth factor-beta; ds.  
XX Homo sapiens.  
OS

XX JPI1326328-A.  
XX 26-NOV-1999.  
XX 13-MAY-1998; 98JP-0130378.  
XX 13-MAY-1998; 98JP-0130378.  
XX (MATSU) MATSUMOTO K.  
XX WPI; 2000-078337/07.  
XX P-PSDB; AAY59451.  
XX Screening a substance which inhibits combination of the X-linked  
XX inhibitor of apoptosis protein  
XX Disclosure; Page 28-30; 43pp; Japanese.  
XX This sequence encodes the human XIAP protein.  
XX The invention relates to a method for screening a substance inhibiting  
XX the formation of a complex between XIAP and TAB1, in which X-linked  
XX inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
XX activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be  
XX tested are contacted with each other and then the presence or formation  
XX of a complex between XIAP and TAB1 is detected. The substance can be used  
XX as a drug for extracellular matrix protein production enhancement, cell  
XX growth inhibition, monocyte migration, physiologically active substance  
XX induction, immunosuppression, and beta-amyloid protein deposition. A  
XX substance inhibiting the formation of a complex between TAB1 and XIAP as  
XX well as between XIAP and TGF-beta (Transforming growth factor-beta) type  
XX I and/or type II receptor is useful as a drug.  
XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
Query Match 100.0%; Score 138; DB 21; Length 1659;  
Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 60  
DB 1396 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCGAAATCTGTATGATAGAAATATT 1455  
QY 61 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120  
DB 1456 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1515  
QY 121 GACAAGTGTCCCATGTGC 138  
DB 1516 GACAAGTGTCCCATGTGC 1533  
RESULT 7  
AAK99405  
ID AAK99405 standard; DNA; 2404 BP.  
XX AC AAK99405;  
XX DT 27-JUN-2002 (first entry)  
XX DE DNA of APP related human homologue hcp35211.  
XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;  
XX amyloid precursor protein; tissue-specific expression control; human APP;  
XX APP pathway modulator; gene therapy; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 692..1528  
XX /tag= a  
XX /product= "Protein of human homologue hcp35211"  
XX /note= "No start codon"



antisense; antiinflammatory; cytostatic; tumour; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 34..1527

FT /\*tag- a

FT /product= "X-linked inhibitor of apoptosis"

XX US6087173-A.

XX PD 11-JUL-2000.

XX PF 09-SEP-1999; 99US-0392580.

XX PR '09-SEP-1999; 99US-0392580.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Cowsett LM, Ackermann EJ;

XX WPI; 2000-498201/44.

XX DR P-PSDB; AAY99985.

XX Antisense compound useful for research reagents, diagnostics,  
PT prophylaxis and for treating disorders associated with X-linked  
PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of  
PT apoptosis

XX Example 13; Column 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to  
CC inhibit expression of the human X-linked inhibitor of apoptosis. The  
CC present sequence is the X-linked inhibitor of apoptosis DNA.  
CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are  
CC more effective inhibitors than unmodified oligonucleotides. The  
CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis  
CC expression in cells and tissues in vitro. The oligonucleotides are also  
CC useful for treating animals or humans, prone to a disease associated  
CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be  
CC used prophylactically to prevent infection, inflammation or tumour  
CC formation.

XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

Query Match 100.0%; Score 138; DB 21; Length 2540;

Best Local Similarity 100.0%; Pred. No. 1.5e-33;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAGGCGCCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60

DB 1348 GAGCAGCTAGGCGCCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 1407

QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120

DB 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1467

QY 121 GACAAGTGTCCTCATGTGC 138

DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 10

ABK93869

ID ABK93869 standard; cDNA; 2540 BP.

XX AC ABK93869;

XX 26-AUG-2002 (first entry)

XX Human cDNA encoding inhibitor of apoptosis, XIAP #1.

XX Human; ss; gene; antisense; inhibitor of apoptosis; XIAP1; XIAP2; XIAP;

KW

XX

KW

XX

KW

XX

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

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PA

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PI

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DR

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DR

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cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
pancreatic cancer; embryonic development; viral pathogenesis;  
autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
lupus erythematosus; herpes virus infection; pox virus infection;  
adenovirus infection; proliferative disease.

Homo sapiens.

WO200228968-A2.

04-APR-2002.

27-SEP-2001; 2001WO-CA01379.

28-SEP-2000; 2000US-0672717.

(UYOT-) UNIV OTTAWA.

(AEGE-) AEGERA THERAPEUTICS INC.

Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

WPI; 2002-479562/51.

P-PSDB; ABG65663.

Novel antisense inhibitor of apoptosis nucleic acid useful for  
enhancing apoptosis in a cell, for treating cancer and other  
proliferative diseases

Disclosure; Fig 1; 135pp; English.

The invention relates to an inhibitor of apoptosis (IAP) antisense  
nucleic acid (1) that inhibits IAP biological activity, regardless of  
length of the antisense nucleic acid, the IAP proteins may be mouse  
or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
composition comprising a mammalian IAP antisense molecule and a method of  
enhancing apoptosis in a cell, comprising administering a negative  
regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
antisense inhibitor is useful for enhancing apoptosis in a cell in a  
mammal diagnosed with a proliferative disease. The method is useful for  
treating a patient diagnosed with a proliferative disease like cancer.  
The IAP antisense molecule is useful to treat, ameliorate, improve,  
sustain or prevent proliferative diseases (e.g. ovarian cancer,  
adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
conditions where apoptosis is involved or implicated (e.g. embryonic  
development, viral pathogenesis, autoimmune disorders, neurodegenerative  
diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
virus, pox virus and adenovirus). The present sequence is a human IAP  
cDNA sequence.

Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;

Query Match 100.0%; Score 138; DB 24; Length 2540;

Best Local Similarity 100.0%; Pred. No. 1.5e-33;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAGGCGCCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60

DB 1348 GAGCAGCTAGGCGCCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 1407

QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120

DB 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1467

QY 121 GACAAGTGTCCTCATGTGC 138

DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 11

ABK93875

ID ABK93875 standard; cDNA; 3000 BP.

XX AC ABK93875;

XX 26-AUG-2002 (first entry)  
 XX Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
 DE Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
 XX cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
 KW pancreatic cancer; embryonic development; viral pathogenesis;  
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
 KW lupus erythematosus; herpes virus infection; pox virus infection;  
 KW adenovirus infection; proliferative disease.  
 XX Homo sapiens.  
 OS  
 XX WO200226968-A2.  
 PN  
 XX 04-APR-2002.  
 PD  
 XX 27-SEP-2001; 2001WO-CA01379.  
 PF  
 XX 28-SEP-2000; 2000US-0672717.  
 PR  
 XX (UYOT-) UNIV OTTAWA.  
 PA  
 XX (AEGE-) AEGERA THERAPEUTICS INC.  
 PI  
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
 XX WPI; 2002-479562/51.  
 DR  
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
 PT enhancing apoptosis in a cell, for treating cancer and other  
 PT proliferative diseases  
 XX  
 PS Example 2; Fig 15; 135pp; English.  
 XX  
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
 CC length of the antisense nucleic acid, the IAP proteins may be mouse  
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
 CC composition comprising a mammalian IAP antisense molecule and a method of  
 CC enhancing apoptosis in a cell, comprising administering a negative  
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
 CC mammal diagnosed with a proliferative disease. The method is useful for  
 CC treating a patient diagnosed with a proliferative disease like cancer.  
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
 CC adenocarcinoma, lymphoma, pancreatic cancer) and also in diseases or  
 CC conditions where apoptosis is involved or implicated (e.g. embryonic  
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
 CC virus, pox virus and adenovirus). The present sequence is a human IAP  
 CC cDNA sequence.  
 XX  
 SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;  
 Query Match 100.0%; Score 138; DB 24; Length 3000;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-33;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
 DB 2004 GAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 2063  
 QY 61 GCTATCGTTTGTCTTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120  
 DB 2064 GCTATCGTTTGTCTTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 2123  
 QY 121 GACAAGTGCCCATGTGC 138  
 DB 2124 GACAAGTGCCCATGTGC 2141

RESULT 12  
 AAV55038  
 ID AAV55038 standard; cDNA; 5232 BP.  
 XX  
 AC AAV55038;  
 XX  
 DT 13-NOV-1998 (first entry)  
 XX  
 DE Human XIAP coding sequence.  
 XX  
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 34..1527  
 FT /\*tag= a  
 FT /product= XIAP  
 XX  
 PN WO9835693-A2.  
 XX  
 XX 20-AUG-1998.  
 PD  
 XX 13-FEB-1998; 98WO-IB00781.  
 PF  
 XX 13-FEB-1997; 97US-0800929.  
 PR  
 XX (UYOT-) UNIV OTTAWA.  
 PA  
 XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
 PI Tsang B;  
 XX  
 DR WPI; 1998-467164/40.  
 DR P-PSDB; AAW69294.  
 XX  
 CC Inducing apoptosis in proliferative mammalian cells with inhibitor  
 CC of IAP or NAIP polypeptide - also methods for prognosis based on  
 CC presence of IAP and NAIP, specifically applied to cancers involving  
 CC p53 mutations  
 XX  
 PS Claim 13; Fig 1; 147pp; English.  
 XX  
 CC This sequence encodes the human XIAP protein, which is an inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC resistance to chemotherapeutic agents and mutations in p53 (it is  
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
 CC genes). Transgenic animals are used for testing the effects of antisense  
 CC oligonucleotides and for screening for the inhibitors.  
 XX  
 SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;  
 Query Match 100.0%; Score 138; DB 19; Length 5232;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-33;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
 DB 1348 GAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 1407  
 QY 61 GCTATCGTTTGTCTTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120  
 DB 1408 GCTATCGTTTGTCTTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 1467

QY 121 GACAGTGTCCCATGTGC 138  
|||||  
DB 1468 GACAGTGTCCCATGTGC 1485

## RESULT 13

ABA48694/c  
ID ABA48694 standard; DNA; 148 BP.

XX ABA48694;

DT 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #7389.

XX Human; microarray; single exon probe; gene expression; breast;

KW disease; cancer; ss.

XX Homo sapiens.

OS WO200157271-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -

XX Claim 4; SEQ ID NO 7389; 327pp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting  
CC the probes with a collection of detectably labelled nucleic acids  
CC derived from mRNA of human breast, and then measuring the label  
CC bound to each probe of the microarray. The probes are useful for  
CC verifying the expression of regions of genomic DNA predicted to  
CC encode proteins. They are useful for gene discovery, and for  
CC determining predisposition and/or prognosing breast disease. Gene  
CC expression analysis is useful for assessing the toxicity of chemical  
CC agents on cells. The microarray of this invention presents a far greater  
CC diversity of probes for measuring gene expression, with far less bias  
CC than expressed sequence tag microarrays. The method is suitable for  
CC rapid production of functional information from genomic sequence. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 148 BP; 43 A; 36 C; 25 G; 44 T; 0 other;

Query Match 97.1%; Score 134; DB 22; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 GACAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
|||||

DB 134 GACAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 75  
QY 61 GCTATCGTTTGTCTTCTGACATCTAGTGCACCTTGTAAACAATGCTGCTGAAGCAGTT 120  
|||||  
DB 74 GCTATCGTTTGTCTTCTGACATCTAGTGCACCTTGTAAACAATGCTGCTGAAGCAGTT 15  
|||||

QY 121 GACAGTGTCCCAT 134  
|||||

DB 14 GACAGTGTCCCAT 1

## RESULT 14

AAI21530/c

ID AAI21530 standard; DNA; 148 BP.

XX AAI21530;

AC 12-OCT-2001 (first entry)

DT Probe #11463 for gene expression analysis in human cervical cell sample.

XX Probe: human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

OS Homo sapiens.

PN WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00670.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human cervical epithelial cells -

XX Claim 25; SEQ ID NO 11463; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes  
CC (SENPs). The present sequence is one such probe. The SENPs are derived  
CC from human HeLa cells. The SENPs can be used to produce a single exon  
CC microarray, which can be used for measuring human gene expression in a  
CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging  
CC of diseases of the cervix, notably cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 148 BP; 43 A; 36 C; 25 G; 44 T; 0 other;

Query Match 97.1%; Score 134; DB 22; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
|||||

DB 134 GACAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 75  
|||||

QY 61 GCTATCGTTTGTCTTCTGACATCTAGTGCACCTTGTAAACAATGCTGCTGAAGCAGTT 120  
|||||

Db 74 GCTATCGTTTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGTCGAGCAGTT 15  
QY 121 GACAAGTGCCCAT 134  
Db 14 GACAAGTGCCCAT 1

RESULT 15  
AAI07226/c  
ID AAI07226 standard; DNA; 148 BP.  
XX  
AC AAI07226;  
XX  
DT 09-OCT-2001 (first entry)  
XX  
DE Probe #7217 used to measure gene expression in human breast sample.  
XX  
KW Probe; human; breast disease; breast cancer; development disorder; ss;  
KW inflammatory disease; Proliferative breast disease; non-carcinoma tumour.  
XX

OS Homo sapiens.

PN WO200157270-A2.

XX  
PD 09-AUG-2001.

XX  
PF 29-JAN-2001; 2001WO-US00661.

XX  
PR 04-FEB-2000; 2000US-0180312.

XX  
PR 26-MAY-2000; 2000US-0207456.

XX  
PR 30-JUN-2000; 2000US-0608408.

XX  
PR 03-AUG-2000; 2000US-0632366.

XX  
PR 21-SEP-2000; 2000US-0234687.

XX  
PR 27-SEP-2000; 2000US-0236359.

XX  
PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX Novel single exon nucleic acid probe used to measuring gene expression

XX in a human breast.

XX Claim 25; SEQ ID No 7217; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes.

XX The present sequence is one such probe. The probes are useful for

XX measuring human gene expression in a human breast sample, where the probe

XX hybridises at high stringency to a nucleic acid expressed in the human

XX breast. The probes are useful for predicting, diagnosing, grading,

XX staging, monitoring and prognosing diseases of the human breast,

XX particularly those diseases with polygenic aetiology. The diseases

XX include: breast cancer, disorders of development, inflammatory diseases

XX of the breast, fibrocystic changes, proliferative breast disease and

XX non-carcinoma tumours.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 148 BP; 43 A; 36 C; 25 G; 44 T; 0 other;

Query Match 97.1%; Score 134; DB 22; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAGGGCGCTTGGACGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60

Db 134 GAGCAGCTAAGGGCGCTTGGACGAGGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 75

QY 61 GCTATCGTTTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGTCGAGCAGTT 120

Db 74 GCTATCGTTTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGTCGAGCAGTT 15  
QY 121 GACAAGTGCCCAT 134  
Db 14 GACAAGTGCCCAT 1

Search completed: April 15, 2003, 21:45:30  
Job time : 93.2396 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	138	100.0	1588	4	US-09-239-867-3
2	138	100.0	2540	2	US-08-511-485-3
3	138	100.0	2540	3	US-09-392-580-1
4	138	100.0	5232	3	US-09-213-971-3
5	138	100.0	5232	3	US-08-800-929A-3
6	138	100.0	5232	4	US-09-617-053A-3
7	125.2	90.7	2100	2	US-08-511-485-9
8	125.2	90.7	2691	3	US-09-213-971-9
9	125.2	90.7	2691	3	US-08-800-929A-9
10	125.2	90.7	2691	4	US-09-617-053A-9
11	119.4	86.5	152331	3	US-09-128-155-16
12	119.4	86.5	176373	3	US-09-128-155-17
13	117.2	84.9	711	3	US-09-121-979-3
14	117.2	84.9	711	4	US-09-332-319-3
15	117.2	84.9	1559	4	US-09-239-867-1
16	61.2	44.3	2862	4	US-08-569-749-13
17	61.2	44.3	2862	5	PGT-US96-12860-13
18	61.2	44.3	3151	3	US-09-213-971-13
19	61.2	44.3	3151	3	US-08-800-929A-13
20	61.2	44.3	3151	4	US-09-617-053A-13
21	58.6	42.5	2601	4	US-08-569-749-3
22	58.6	42.5	2601	5	PGT-US96-12860-3
23	58.6	42.5	2676	3	US-09-213-971-11
24	58.6	42.5	2676	3	US-08-800-929A-11
25	58.6	42.5	2676	4	US-09-617-053A-11
26	58.6	42.5	3076	2	US-09-203-144-1
27	58.6	42.5	6669	3	US-09-213-971-5



ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2540 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-511-485-3

Query Match 100.0%; Score 138; DB 2; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 4.4e-37;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCCCTGCAAGAGGAGGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
DB 1348 GAGCAGCTAAGCGCCCTGCAAGAGGAGGAGCTTTGCAAAATCTGTATGATAGAAATATT 1407  
QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120  
DB 1408 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467  
QY 121 GACAAGTGTCCTCATGTGC 138  
DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 3  
US-09-392-580-1  
Sequence 1, Application US/09392580  
Patent No. 6087173  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION  
FILE REFERENCE: RTS-0072  
CURRENT APPLICATION NUMBER: US/09/392,580  
CURRENT FILING DATE: 1999-09-09  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 1  
LENGTH: 2540  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (34)..(1527)  
US-09-392-580-1

Query Match 100.0%; Score 138; DB 3; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 4.4e-37;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCCCTGCAAGAGGAGGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
DB 1348 GAGCAGCTAAGCGCCCTGCAAGAGGAGGAGCTTTGCAAAATCTGTATGATAGAAATATT 1407  
QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120  
DB 1408 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467  
QY 121 GACAAGTGTCCTCATGTGC 138  
DB 1468 GACAAGTGTCCTCATGTGC 1485

## RESULT 4

US-09-212-971-3  
Sequence 3, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5232  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4623)...(4623)  
OTHER INFORMATION: n can be any nucleotide  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4622)...(4622)  
OTHER INFORMATION: n can be any nucleotide  
US-09-212-971-3

Query Match 100.0%; Score 138; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 5.7e-37;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCCTGCAAGAGGAGGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
DB 1348 GAGCAGCTAAGCGCCCTGCAAGAGGAGGAGCTTTGCAAAATCTGTATGATAGAAATATT 1407  
QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120  
DB 1408 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467  
QY 121 GACAAGTGTCCTCATGTGC 138  
DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 5  
US-08-800-929A-3

Sequence 3, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 28-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...5232  
OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

US-08-800-929A-3  
Query Match 100.0%; Score 138; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 5.7e-37;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGGCGCTGCGAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
Db 1348 GAGCAGCTAAGGCGCTGCGAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1407  
QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120  
Db 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467  
QY 121 GACAAGTGTCCTCATGTGC 138  
Db 1468 GACAAGTGTCCTCATGTGC 1485  
RESULT 6

US-09-617-053A-3  
Sequence 3, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 5232  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4623)...(4623)  
OTHER INFORMATION: n can be any nucleotide  
NAME/KEY: variation  
LOCATION: (4622)...(4622)  
OTHER INFORMATION: n can be any nucleotide  
US-09-617-053A-3  
Query Match 100.0%; Score 138; DB 4; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 5.7e-37;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGGCGCTGCGAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
Db 1348 GAGCAGCTAAGGCGCTGCGAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1407  
QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120  
Db 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467  
QY 121 GACAAGTGTCCTCATGTGC 138  
Db 1468 GACAAGTGTCCTCATGTGC 1485  
RESULT 7  
US-08-511-485-9  
Sequence 9, Application US/08511485  
Patent No. 5915912  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/511,485  
;; FILING DATE: 04-AUG-1995  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 07540/002001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617/542-5070  
;; TELEFAX: 617/542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2100 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: DNA (genomic)  
US-08-511-485-9

Query Match 90.7%; Score 125.2; DB 2; Length 2100;  
Best Local Similarity 94.2%; Pred. NO. 8.2e-33;  
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
DB 1438 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1497  
  
QY 61 GCTATCGTTTTTCTTCTGTGGACATCTAGTACATGTAAACAATGTCTGAAGCAGTT 120  
DB 1498 GCTATCGTTTTTCTTCTGTGGACATCTAGTACATGTAAACAATGTCTGAAGCAGTT 1557  
  
QY 121 GACAAAGTGTCCCATGTGC 138  
DB 1558 GACAAATGTCCCATGTGC 1575

RESULT 8  
US-09-212-971-9  
;; Sequence 9, Application US/09212971B  
;; Patent No. 6107041  
;; GENERAL INFORMATION:  
;; APPLICANT: Korneluk, Robert G  
;; APPLICANT: Mackenzie, Alexander E  
;; APPLICANT: Liston, Peter  
;; APPLICANT: Baird, Stephen  
;; APPLICANT: Tsang, Benjamin K  
;; APPLICANT: Pratt, Christine  
;; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
;; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
;; FILE REFERENCE: 07891/009002  
;; CURRENT APPLICATION NUMBER: US/09/212,971B  
;; CURRENT FILING DATE: 1998-12-16  
;; EARLIER APPLICATION NUMBER: 60/017,354  
;; EARLIER FILING DATE: 1996-04-26  
;; EARLIER APPLICATION NUMBER: 60/030,590  
;; EARLIER FILING DATE: 1996-11-14  
;; EARLIER APPLICATION NUMBER: 08/800,929  
;; EARLIER FILING DATE: 1997-02-13  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 9  
;; LENGTH: 2691  
;; TYPE: DNA  
;; ORGANISM: Mus musculus  
US-09-212-971-9

Query Match 90.7%; Score 125.2; DB 3; Length 2691;  
Best Local Similarity 94.2%; Pred. NO. 8.9e-33;  
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
DB 1983 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042  
  
QY 61 GCTATCGTTTTTCTTCTGTGGACATCTAGTACATGTAAACAATGTCTGAAGCAGTT 120  
DB 2043 GCTATCGTTTTTCTTCTGTGGACATCTAGTACATGTAAACAATGTCTGAAGCAGTT 2102  
  
QY 121 GACAAAGTGTCCCATGTGC 138  
DB 2103 GACAAATGTCCCATGTGC 2120

RESULT 9  
US-08-800-929A-9  
;; Sequence 9, Application US/08800929A  
;; Patent No. 6133437  
;; GENERAL INFORMATION:  
;; APPLICANT: Korneluk, Robert G  
;; APPLICANT: Mackenzie, Alexander E  
;; APPLICANT: Liston, Peter  
;; APPLICANT: Baird, Stephen  
;; APPLICANT: Tsang, Benjamin K  
;; APPLICANT: Pratt, Christine  
;; TITLE OF INVENTION: DETECTION AND MODULATION OF  
;; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
;; NUMBER OF SEQUENCES: 17  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Clark & Eibing LLP  
;; STREET: 176 Federal Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/800,929A  
;; FILING DATE: 13-FEB-1997  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/030,590  
;; FILING DATE: 14-NOV-1996  
;; APPLICATION NUMBER: 60/017,354  
;; FILING DATE: 26-APR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bieker-Brady, Kristina  
;; REGISTRATION NUMBER:  
;; REFERENCE/DOCKET NUMBER: 07891/009001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-428-0200  
;; TELEFAX: 617-428-7045  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2691 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
US-08-800-929A-9

Query Match 90.7%; Score 125.2; DB 3; Length 2691;  
Best Local Similarity 94.2%; Pred. NO. 8.9e-33;  
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
DB 1983 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042

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QY 61 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120
|||||
DB 2043 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 2102
|||||
QY 121 GACAAGTGCCCATGTGC 138
|||||
DB 2103 GACAAATGTCCCATGTGC 2120

RESULT 10
US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 90.7%; Score 125.2; DB 4; Length 2691;
Best Local Similarity 94.2%; Pred. No. 8.9e-33;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
DB 1983 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042
|||||
QY 61 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120
|||||
DB 2043 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 2102
|||||
QY 121 GACAAGTGCCCATGTGC 138
|||||
DB 2103 GACAAATGTCCCATGTGC 2120

RESULT 11
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16/c

Query Match 86.5%; Score 119.4; DB 3; Length 176373;
Best Local Similarity 92.0%; Pred. No. 3.3e-30;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
DB 13011 GAGCAGCTAAGCACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 13070
|||||
QY 61 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120
|||||
DB 13071 GCTGTCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 13130
|||||
QY 121 GACAAGTGCCCATGTGC 137
|||||
DB 13131 GACAAATGTCTCAGTG 13147

RESULT 13
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 86.5%; Score 119.4; DB 3; Length 152331;
Best Local Similarity 92.0%; Pred. No. 3.3e-30;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
DB 24123 GAGCAGCTAAGCACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 24064
|||||
QY 61 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120
|||||
DB 24063 GCTGTCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 24004
|||||
QY 121 GACAAGTGCCCATGTGC 137
|||||
DB 24003 GACAAATGTCTCAGTG 23987

RESULT 12
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 86.5%; Score 119.4; DB 3; Length 176373;
Best Local Similarity 92.0%; Pred. No. 3.3e-30;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
DB 13011 GAGCAGCTAAGCACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 13070
|||||
QY 61 GCTATCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120
|||||
DB 13071 GCTGTCGTTTGTTCCTGTGGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 13130
|||||
QY 121 GACAAGTGCCCATGTGC 137
|||||
DB 13131 GACAAATGTCTCAGTG 13147

RESULT 13
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
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GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Holcik, Martin  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF  
; FILE REFERENCE: 07891/021001  
; CURRENT APPLICATION NUMBER: US/09/121,979  
; CURRENT FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-121-979-3

Query Match 84.9%; Score 117.2; DB 3; Length 711;  
Best Local Similarity 90.6%; Pred. No. 2.7e-30;  
Matches 125; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60  
Db 532 GAGCCGCTAAGCGCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 591  
QY 61 GCTATCGTTTTCCTTGTGGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120  
Db 592 GCTGTGTTTTCCTTGTGGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 651  
QY 121 GACAGATGCCCATGTGC 138  
Db 652 GACAGATGCCCATGTGC 669

## RESULT 14

US-09-332-319-3  
; Sequence 3, Application US/09332319  
; Patent No. 6171821  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Holcik, Martin  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF  
; FILE REFERENCE: 07891/021002  
; CURRENT APPLICATION NUMBER: US/09/332,319  
; CURRENT FILING DATE: 1999-06-14  
; EARLIER APPLICATION NUMBER: 09/121,979  
; EARLIER FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-332-319-3

Query Match 84.9%; Score 117.2; DB 4; Length 711;  
Best Local Similarity 90.6%; Pred. No. 2.7e-30;  
Matches 125; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60  
Db 532 GAGCCGCTAAGCGCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 591  
QY 61 GCTATCGTTTTCCTTGTGGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120  
Db 592 GCTGTGTTTTCCTTGTGGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 651  
QY 121 GACAGATGCCCATGTGC 138  
Db 652 GACAGATGCCCATGTGC 669

## RESULT 15

US-09-239-867-1  
; Sequence 1, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; TITLE OF INVENTION: MALE FERTILITY  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1559  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)-(1559)  
; OTHER INFORMATION: n - A,T,C or G  
US-09-239-867-1

Query Match 84.9%; Score 117.2; DB 4; Length 1559;  
Best Local Similarity 90.6%; Pred. No. 3.6e-30;  
Matches 125; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGCGCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60  
Db 1322 GAGCCGCTAAGCGCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 1381  
QY 61 GCTATCGTTTTCCTTGTGGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120  
Db 1382 GCTGTGTTTTCCTTGTGGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 1441  
QY 121 GACAGATGCCCATGTGC 138  
Db 1442 GACAGATGCCCATGTGC 1459

Search completed: April 16, 2003, 00:58:51  
Job time : 54.3698 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 33.1823 Seconds  
(without alignments)  
3648.005 Million cell updates/sec

Title: US-09-654-743-48  
Perfect score: 138  
Sequence: 1 ggcagcctaagcgctgcga.....ttgacaagtgtcccatgtgc 138

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.\*

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2: /cgn2.6/pdata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2.6/pdata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2.6/pdata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2.6/pdata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2.6/pdata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2.6/pdata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2.6/pdata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2.6/pdata/2/pubpna/US09\_NEW\_PUB.seq.\*  
10: /cgn2.6/pdata/2/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2.6/pdata/2/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2.6/pdata/2/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2.6/pdata/2/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2.6/pdata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	138	100.0	2404	9	US-09-964-899-38
3	138	100.0	2540	9	US-09-201-936-3
4	138	100.0	5232	10	US-09-974-592-3
5	134	97.1	148	10	US-09-864-761-30419
6	125.2	90.7	2100	9	US-09-201-936-9
7	125.2	90.7	2691	10	US-09-974-592-9
8	119.4	86.5	152331	9	US-10-095-407-16
9	119.4	86.5	176373	9	US-10-095-407-17
10	61.2	44.3	2416	9	US-09-201-936-41
11	61.2	44.3	3151	10	US-09-974-592-13
12	60.2	43.6	2450	9	US-09-201-936-39
13	58.6	42.5	2676	10	US-09-974-592-11
14	58.6	42.5	3076	9	US-09-954-531-16
15	58.6	42.5	3076	10	US-09-954-456-1635
16	58.6	42.5	6669	10	US-09-974-592-5
17	57	41.3	460	10	US-09-960-352-8049
18	57	41.3	2676	9	US-09-201-936-5
19	54.8	39.7	2580	9	US-09-201-936-7

20	54.8	39.7	3532	10	US-09-880-107-3354
21	54.8	39.7	3732	10	US-09-974-592-7
C 22	33	23.9	456	10	US-09-770-444-524
23	32	23.2	1992	9	US-09-949-842-2
C 24	32	23.2	8847	9	US-10-092-154-995
C 25	32	23.2	8847	10	US-09-764-847-995
26	30.2	21.9	360	12	US-10-033-078-17
27	29.6	21.4	9139	10	US-09-965-553-22
28	29.2	21.2	5744	10	US-09-764-877-3507
C 29	28.8	20.9	32193	9	US-09-764-868-1508
30	28.8	20.9	98865	10	US-09-770-689A-3
31	28.8	20.9	173808	12	US-10-003-806-10
32	28.6	20.7	629	10	US-09-917-800A-885
C 33	28.6	20.7	197456	9	US-09-877-177-10
C 34	28.4	20.6	336	10	US-09-960-352-9169
35	28.4	20.6	4232	10	US-09-070-927A-71
C 36	28.2	20.4	924	9	US-09-738-626-769
C 37	28.2	20.4	3309400	9	US-09-738-626-1
C 38	28	20.3	306	9	US-09-796-692-4055
C 39	28	20.3	368004	10	US-09-949-654-3
C 40	27.8	20.1	2127	10	US-09-974-300-1668
41	27.6	20.0	1023	9	US-09-938-842A-2411
42	27.6	20.0	2811	9	US-09-938-842A-2538
43	27.6	20.0	6417	10	US-09-764-877-3505
C 44	27.6	20.0	20165	9	US-10-199-330-7
C 45	27.6	20.0	20165	9	US-10-199-334-7

## ALIGNMENTS

## RESULT 1

US-09-864-761-13853/c  
; Sequence 13853, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 13853  
LENGTH: 489  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL022156.1  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8  
US-09-864-761-13853

Query Match 100.0%; Score 138; DB 10; Length 489;  
Best Local Similarity 100.0%; Pred. No. 4.6e-35;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACAGCTAAGGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
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DB 450 GACAGCTAAGGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGGATAGAAATATT 391  
QY 61 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120  
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DB 390 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 331  
QY 121 GACAAGTGTCCTCATGTGC 138  
|||||  
DB 330 GACAAGTGTCCTCATGTGC 313

RESULT 2  
US-09-964-899-38  
Sequence 38, Application US/09964899  
Patent No. US20020174446A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Dalia et al.  
TITLE OF INVENTION: Identification of Genes Involved in  
Alzheimer's Disease Using Drosophila Melanogaster  
FILE REFERENCE: 4-31612 A  
CURRENT APPLICATION NUMBER: US/09/964,899  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: 60/236,893  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/298,309  
PRIOR FILING DATE: 2001-06-14  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows version 4.0  
SEQ ID NO 38  
LENGTH: 2404  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-964-899-38

Query Match 100.0%; Score 138; DB 9; Length 2404;  
Best Local Similarity 100.0%; Pred. No. 9.6e-35;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACAGCTAAGGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
|||||  
DB 1349 GACAGCTAAGGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGGATAGAAATATT 1408  
QY 61 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120  
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DB 1409 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 1468

QY 121 GACAAGTGTCCTCATGTGC 138  
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DB 1469 GACAAGTGTCCTCATGTGC 1486

RESULT 3  
US-09-201-936-3  
Sequence 3, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: MacKenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 2540  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (2540)....(2540)  
OTHER INFORMATION: N may be any nucleotide  
US-09-201-936-3

Query Match 100.0%; Score 138; DB 9; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 9.8e-35;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACAGCTAAGGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
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DB 1348 GACAGCTAAGGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGGATAGAAATATT 1407  
QY 61 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 120  
|||||  
DB 1408 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTGTAAACAATGTGCTGAAGCAGTT 1467  
QY 121 GACAAGTGTCCTCATGTGC 138  
|||||  
DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 4  
US-09-974-592-3  
Sequence 3, Application US/09974592  
Patent No. US20020120121A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: MacKenzie, Alexander E.  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
THEIR EXPRESSION  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF\*PROLIFERATIVE  
DISEASE  
FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592





; LENGTH: 2100  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-201-936-9

Query Match 90.7%; Score 125.2; DB 9; Length 2100;  
Best Local Similarity 94.2%; Pred. No. 1.2e-30;  
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
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Db 1438 GAGCAGCTAAGGCGCTACAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1497  
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QY 61 GCTATCGTTTTTCTCTGTCACATCTAGTCACCTGTAAACAATCTGCTGAAGCAGTT 120  
|||||  
Db 1498 GCTATCGTTTTTCTCTGTCACATCTAGTCACCTGTAAACAATCTGCTGAAGCAGTT 1557  
|||||  
QY 121 GACAAGTGTCCTCATGTGC 138  
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Db 1558 GACAAATGTCCCATGTGC 1575  
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## RESULT 7

US-09-974-592-9

; Sequence 9, Application US/09974592

; Patent No. US20020120121A1

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND

; TITLE OF INVENTION: NALP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: DISEASE

; FILE REFERENCE: 07891/009004

; CURRENT APPLICATION NUMBER: US/09/974,592

; CURRENT FILING DATE: 2001-10-09

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/800,929

; PRIOR FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2691

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-974-592-9

Query Match 90.7%; Score 125.2; DB 10; Length 2691;  
Best Local Similarity 94.2%; Pred. No. 1.4e-30;  
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
|||||  
Db 1983 GAGCAGCTAAGGCGCTACAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042  
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QY 61 GCTATCGTTTTTCTCTGTCACATCTAGTCACCTGTAAACAATCTGCTGAAGCAGTT 120  
|||||  
Db 2043 GCTATCGTTTTTCTCTGTCACATCTAGTCACCTGTAAACAATCTGCTGAAGCAGTT 2102  
|||||  
QY 121 GACAAGTGTCCTCATGTGC 138  
|||||  
Db 2103 GACAAATGTCCCATGTGC 2120  
|||||

## RESULT 8

US-10-095-407-16/c

; Sequence 16, Application US/10095407

; Patent No. US20020164330A1

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/10/095,407  
; CURRENT FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/091,650  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/054,646  
; PRIOR FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 152331  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(152331)  
; OTHER INFORMATION: n - A,T,C or G  
US-10-095-407-16

Query Match 86.5%; Score 119.4; DB 9; Length 152331;  
Best Local Similarity 92.0%; Pred. No. 6.6e-28;  
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
|||||  
Db 24123 GAGCAGCTAAGACACCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 24064  
|||||  
QY 61 GCTATCGTTTTTCTCTGTCACATCTAGTCACCTGTAAACAATCTGCTGAAGCAGTT 120  
|||||  
Db 24063 GCTGTCGTTTTTCTCTGTCACATCTAGTCACCTGTAAACAATCTGCTGAAGCAGTT 24004  
|||||  
QY 121 GACAAGTGTCCTCATGTGC 137  
|||||  
Db 24003 GACAAATGTCTCAAGTG 23987  
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## RESULT 9

US-10-095-407-17

; Sequence 17, Application US/10095407

; Patent No. US20020164330A1

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; FILE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/10/095,407

; CURRENT FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/091,650

; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: US 60/054,646

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 176373

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(176373)

; OTHER INFORMATION: n - A,T,C or G

US-10-095-407-17

Query Match 86.5%; Score 119.4; DB 9; Length 176373;  
Best Local Similarity 92.0%; Pred. No. 7e-28;  
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
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Db 13011 GAGCAGCTAAGACACCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 13070  
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FILE REFERENCE: 07891/009004  
CURRENT APPLICATION NUMBER: US/09/974,592



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Db 2480 AGAAGTGTCCCTATTG 2496

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Job time : 70.1823 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 660.292 Seconds  
(without alignments)  
3384.833 Million cell updates/sec

Title: US-09-654-743-48  
Perfect score: 138  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 21	67	48.6	634	13	BM533524
C 22	66.6	48.3	511	12	BF610755
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24	65	47.1	456	10	BE468783
25	65	47.1	640	14	BQ097223
C 26	65	47.1	673	13	BJ045197
27	65	47.1	816	14	BQ097355
C 28	64.4	46.7	771	12	BF724041
C 29	64.4	46.7	976	9	AO091115
C 30	63.4	45.9	615	13	BM438676
C 31	63.4	45.9	647	12	BF610861
C 32	63.2	45.8	583	13	BJ097423
33	61.2	44.3	400	12	BF452698
C 34	61.2	44.3	451	13	BM190727
35	61.2	44.3	467	10	AW988289
36	61.2	44.3	471	9	AA172848
C 37	61.2	44.3	522	10	BE577966
C 38	61.2	44.3	522	13	BM260985
39	61.2	44.3	564	13	BM191198
40	61.2	44.3	565	10	AW640116
C 41	61.2	44.3	568	14	BQ386511
C 42	61.2	44.3	597	14	BQ569086
C 43	61.2	44.3	605	13	BM260905
C 44	61.2	44.3	618	10	BE578881
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#### ALIGNMENTS

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DEFINITION  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

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CM2-CT5003-051000-408-g04 CT5003 Homo sapiens CDNA, mRNA sequence.  
BF754025.1 GI:12080701  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 446)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsumura,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-CF5003-051000-408-904&tl3=2000-10-05&tl4=1)  
 Seg primer: puc 18 forward  
 High quality sequence start: 6  
 High quality sequence stop: 446.

## FEATURES

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BASE COUNT 145 a 94 c 69 g 138 t

ORIGIN

Query Match 100.0%; Score 138; DB 12; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-32;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAAATATT 60
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DB 358 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAAATATT 299
    |||||||

QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 120
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DB 298 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 239
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QY 121 GACAAGTGCCCATGTGC 138
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DB 238 GACAAGTGCCCATGTGC 221
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## RESULT 2

BQ007511/c  
 LOCUS BQ007511 757 bp mRNA linear EST 26-MAR-2002  
 DEFINITION UI-H-ED1-ayb-b-04-0-UI-s1 NCI-CGAP\_ED1 Homo sapiens cDNA clone IMAGE:5836323 3', mRNA sequence.  
 ACCESSION BQ007511  
 VERSION BQ007511.1 GI:19732411  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 757)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Seg primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

source

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        /db_xref="taxon:9606"
        /clone="IMAGE:5836323"
  
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/clone_lib="NCI-CGAP_ED1"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI-CGAP_ED1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma cell line C8S. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
TAG-LIB-UI-H-ED1
TAG-TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"
BASE COUNT 257 a 141 c 105 g 254 t
ORIGIN
  
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Query Match 100.0%; Score 138; DB 14; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-32;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 653 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAAATATT 594
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QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 120
    |||||||
DB 593 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 534
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QY 121 GACAAGTGCCCATGTGC 138
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DB 533 GACAAGTGCCCATGTGC 516
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RESULT 3  
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 LOCUS BQ007511 784 bp mRNA linear EST 07-MAR-2000  
 DEFINITION t94b02.x1 NCI-CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2285739 3', similar to SW-IAF3\_HUMAN P98170 INHIBITOR OF APOPTOSIS PROTEIN 3', mRNA sequence.  
 ACCESSION BQ007511  
 VERSION BQ007511.1 GI:4664866  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 784)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone Distribution: Washington University Genome Sequencing Center  
 found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 472 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 465  
 POLYA=No.

Site-2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

BASE COUNT	202 a	121 c	148 g	213 t
ORIGIN				
Query Match	94.2%	Score 130;	DB 13;	length 684;
Best Local Similarity	96.4%	Pred. No. 2.3e-29;		
Matches 133;	Conservative	0;	Mismatches 5;	Indels 1
				0: Gaps 0;
QY	1	GAGCAGCTAAGCGCCCTGCAAGAGGAGAGAACTTTGGCAAAATCTGCTATGGATAGAGAAATTT	60	
DB	70	GAGCAGCTAAGCGCCCTGCAAGAGGAGAGAACTTTGGCAAAATCTGCTATGGATAGAGAAATTT	129	
QY	61	GCATATCGTTTTTGTTCCTTGGACATCTAGTCACTTGTAAACAATCTGCTGAAGCAGTT	120	
DB	130	GCATATCGTTTTTGTTCCTTGGACATCTAGTCACTTGTAAACAATCTGCTGAAGCAGTT	189	
QY	121	GACAAGTGTCCCATGTGC	138	
DB	190	GACAATGTCCCATGTGC	207	
RESULT 5				
BB489347				
LOCUS		305 bp	mRNA	linear
DEFINITION	BB489347	RIKEN full-length cDNA clone D530006021.3, similar to U36842 Mus musculus	13 days embryo stomach Mus	EST 23-JUL-2000
		IAP homolog A (MIRA) mRNA, mRNA sequence.		
ACCESSION	BB489347			
VERSION	BB489347.1	GI:9406956		
KEYWORDS				
SOURCE		house mouse.		
ORGANISM		Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
REFERENCE		1 (bases 1 to 305)		
AUTHORS		Konno,H., Alizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saigo,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toyota,T., Tsunoda,Y., Watanishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.		
		RIKEN Mouse ESTs (Konno,H., et al.)		
TITLE		Unpublished (2000)		
JOURNAL		Contact: Yoshihide Hayashizaki		
COMMENT		Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute		
		The Institute of Physical and Chemical Research (RIKEN)		
		1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan		
		Tel: 81-45-503-9222		
		Fax: 81-45-503-9216		
		Email: genome-res@gsr.riken.go.jp		
		URL: http://genome.gsc.riken.go.jp/		
		Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
		Thermotranscription and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)		
		Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.		
		Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)		
		Carninci,P. and Hayashizaki,Y.		
		High-efficiency full-length cDNA cloning. Methods Enzymol. 303,		

M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenhiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki  
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermostabilization and thermoactivation of the thermostable enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

Location/Qualifiers  
1. 221  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone\_lib="D53009D11"  
/clone\_lib="RIKEN full-length enriched, 13 days embryo  
stomach"  
/tissue\_type="stomach"  
/dev\_stage="13 days embryo"  
/lab\_host="DH10B"  
/note="Site:1: Sali; Site:2: BamHI; CDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGCGCGCGCAACTCGAGTCTTTTCTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adaptor of sequence [5'  
GAGAGAGATCTTCGATTAAATAATTAATCCGCCGCCCCC 3']. cDNA  
was cleaved with BamHI and XhoI. Vector: a modified  
pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 67 a 50 c 45 g 59 t  
ORIGIN

Query Match 89.6%; Score 123.6; DB 10; Length 221;  
Best Local Similarity 93.5%; Pred. No. 1.4e-27;  
Matches 129; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GAGCAGCTAGGCGCCCTGCAAGAGGAGAAGCTTTGCAAAATCTGTATGGATAGAAATATT 60  
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Db 61 GAGCACCTAAGGCGCCCTACAGAGGAGAAGCTTTCCAAATCTGTATGGATAGAAATATT 120

QY 61 GCTATCGTTTGTTCCTGTGGACATCTACTCACTTGAACAATGTCCTGAGCAGCTT 120  
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Db 121 GCTATCGTTTGTTCCTGTGGACATCTGTCTACTTGAACAAGCTGTGCGAAGCAGT 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 GACAAGTGTCACATGTGC 138  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 181 GACAATATCCATGTGC 198

RESULT 7



BB493232 306 bp mRNA linear EST 25-JUL-2000  
 LOCUS BB493232 RIKEN full-length enriched, 13 days embryo stomach Mus  
 DEFINITION musculus cDNA clone D530032B07.3 similar to U36842 Mus musculus  
 IAP homolog A (MIHA) mRNA, mRNA sequence.

ACCESSION BB493232.1 GI:9451859  
 VERSION BB493232.1  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 306)  
 AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
 Unpublished (2000)  
 COMMENT Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.go.jp/  
 URL: http://genome.gsc.riken.go.jp/  
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES  
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 /clone\_lib="RIKEN full-length enriched, 13 days embryo stomach"  
 /tissue\_type="stomach"  
 /dev\_stage="13 days embryo"  
 /lab\_host="DH10B"  
 /note="Site\_1: SalI; Site\_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCTCAAGAGAGAGAGCTTTCACAAATCTGTATGATAGAAATATT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

Query Match 89.6%; Score 123.6; DB 10; Length 306;  
 Best Local Similarity 93.5%; pred. No. 1.6e-27;  
 Matches 129; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 GAGAGAGTAAAGCGCGCTCAAGAGAGAGAGCTTTCACAAATCTGTATGATAGAAATATT 50  
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 Db 147 GACCAAGCTCAGCGCGCTCAAGAGAGAGAGCTTTCACAAATCTGTATGATAGAAATATT 206  
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 Oy 61 GCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTCAAGCAGTT 120  
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 Db 207 GCTTCCTGTTTGTTCCTTGTGGACATCTGTCCTTGTAAACAATGTGCTCAAGCAGTT 266  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Oy 121 GACAAGTCTCCCATGTGC 138  
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 Db 267 GACAAATCTCCCATGTGC 284  
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RESULT 8  
 LOCUS BB489976  
 DEFINITION BB489976 RIKEN full-length enriched, 13 days embryo stomach Mus  
 musculus cDNA clone D530012B15.3 similar to U36842 Mus musculus  
 IAP homolog A (MIHA) mRNA, mRNA sequence.

ACCESSION BB489976  
 VERSION BB489976.1 GI:9407585  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 308)  
 AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
 Unpublished (2000)  
 COMMENT Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.go.jp/  
 URL: http://genome.gsc.riken.go.jp/  
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES  
 source Location/Qualifiers  
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 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="D530032B07"  
 /clone\_lib="RIKEN full-length enriched, 13 days embryo stomach"  
 /tissue\_type="stomach"  
 /dev\_stage="13 days embryo"  
 /lab\_host="DH10B"  
 /note="Site\_1: SalI; Site\_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCTCAAGAGAGAGCTTTCACAAATCTGTATGATAGAAATATT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

# FEATURES

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source
1. 308
/organism="Mus musculus"
/location/Qualifiers
/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched, 13 days embryo
stomach"
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/dev_stage="13 days embryo"
/lab_host="DH10B"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATTCGAGTTAAATTAATTCACCCGCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT      88 a      68 c      67 g      85 t
ORIGIN
Query Match      89.6%; Score 123.6; DB 10; Length 308;
Best Local Similarity 93.5%; Pred. No. 1.6e-27;
Matches 129; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGCAGCTAAGCGCTCGAGAGAGAGAGCTTCCAAAATCTGTATGATAGAAATATT 60
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 148 GACCAGCTAAGCGCTCAAGAGAGAGAGCTTCCAAAATCTGTATGATAGAAATATT 207

Qy 61 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTTGTAAACATGCTGAAGCAGCTT 120
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 208 GCTTTTCGTTTTTGTCTGTGACATCTAGTCACCTTGTAAACATGCTGAAGCAGCTT 267

Qy 121 GACAAGTCTCCCATGTC 138
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 268 GACAAATGCCCATGTC 285

RESULT 9
A1418337/c
LOCUS      447 bp      mRNA      linear      EST 09-MAR-1999
DEFINITION      t948a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:211198 3' similar to gb:X55110 MIDKINE PRECURSOR (HUMAN));,
mRNA sequence.
ACCESSION      A1418337
VERSION      A1418337.1 GI:4264268
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.
Seq primer: 40up from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1. 447

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:211198"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT      160 a      75 c      69 g      143 t
ORIGIN
Query Match      89.1%; Score 123; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CTGCAAGAGGAGAGCTTGCAAAATCTGTATGGATAGAAATATTCCTATCGTTTTTGT 75
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Db 447 CTGCAAGAGGAGAGCTTGCAAAATCTGTATGGATAGAAATATTCCTATCGTTTTTGT 388

Qy 76 CTTCTGGACATCTATGTCACCTTGTAAACAATCTGTGAAGCAGCTTGACAAAGTGCCCATG 135
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 CTTCTGGACATCTATGTCACCTTGTAAACAATCTGTGAAGCAGCTTGACAAAGTGCCCATG 328

Qy 136 TGC 138
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Db 327 TGC 325

RESULT 10
BB491005
LOCUS      319 bp      mRNA      linear      EST 25-JUL-2000
DEFINITION      BB491005 RIKEN full-length enriched, 13 days embryo stomach Mus
musculus cDNA clone D530019A07 3' similar to U36842 Mus musculus
IAP homolog A (MHA) mRNA, mRNA sequence.
ACCESSION      BB491005
VERSION      BB491005.1 GI:9449632
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 319)
Kono.H., Aizawa.K., Akahira.S., Akiyama.J., Arakawa.T., Carninci
P., Endo.T., Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N.,
Hirozane.T., Hori.F., Ishii.Y., Ishikawa.J., Ishikawa.T., Itoh.M.,
Izawa.M., Kadota.K., Kagawa.I., Kai.C., Kawai.J., Kikuchi.N.,
Kiyosawa.H., Kojima.Y., Kondo.S., Koya.S., Kurihara.C., Kusakabe.M.,
Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y.,
Ono.T., Owa.C., Saito.H., Sakai.C., Sato.K., Shibata.K., Shibata
Y., Shigemoto.Y., Shinagawa.A., Shiraki.T., Sogabe.Y., Sugahara.Y.,
Suzuki.H., Suzuki.H., Tagawa.A., Takahashi.F., Tomimaga.N., Toya
T., Tsunoda.Y., Watahiki.A., Watanabe.S., Yamamori.T., Yamana.K.,
Yano.R., Yasunishi.A., Yokota.T., Yoshida.K., Yoshiki.A., Yoshino
M., Muramatsu.M. and Hayashizaki.Y.
RIKEN Mouse ESTs (Kono.H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsukuba-shi, Ibaraki 305-8565, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp.

```



```

Db 180 GACGAGCTAAGGCCCTTACAAAGAGAGAGAGCTTTCCAAAATCTGTATGGATAGAAATATT 239
QY 61 CCTATCGTTTGTCTTCTGTGGACATCTAGTCACTTGTAAACAATGCTGGAAGCAGTT 120
Db 240 GCCTTCGTTTGTCTTCTGTGGACATCTGTCTACTTGTAAACAGTGTGCAGAGCAGTT 299
QY 121 GACAAGTGTCCCATGTGC 138
Db 300 GACAAATTCCTCATGTGC 317

RESULT 12
AQ697308/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

AQ697308 560 bp DNA linear GSS 06-JUL-1999
HS 5531.B1.D07.T7A.RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-1107 Col-13 Row-H, DNA sequence.
AQ697308
AQ697308.1 GI:5387556
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 560)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahalras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1107 row: H column: 13
Seq primer: T7
Class: BAC ends
High quality sequence stop: 560.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-1107 Col-13 Row-H"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from a randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 154 a 121 c 90 g 187 t 8 others
ORIGIN
Query Match 85.8%; Score 118.4; DB 17; Length 560;
Best Local Similarity 91.2%; Pred. No. 8e-26;
Matches 125; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
Db 299 GAGCAGCTAAGCAGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 240
QY 61 GCTATCGTTTGTCTTCTGTGGACATCTAGTCACTTGTAAACAATGCTGGAAGCAGTT 120

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Db 239 GCTGCTGTTTATTCCTTGTGGACATCCAGTCACTGCTAAACAATGCTGGAAGTGGT 180
QY 121 GACAAGTGTCCCATGTG 137
Db 179 GACAATGTCTCAAGTG 163

RESULT 13
AV706807
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AV706807 716 bp mRNA linear EST 09-OCT-2000
AV706807 ADB Homo sapiens cDNA clone ADBCOF01 5', mRNA sequence.
AV706807
AV706807.1 GI:10724085
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 716)
Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao
,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBCOF01"
/clone_lib="ADB"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 207 a 148 c 193 g 163 t 5 others
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Best Local Similarity 93.5%; Pred. No. 9.7e-25;
Matches 129; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
Db 515 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 574
QY 61 GCTATCGTTTGTCTTCTGTGGACATCTAGTCACTTGTAAACAATGCTGGAAGCAGTT 120
Db 575 GCTATCGTTTGTGGTCTTGTGGACATCTAGTCACTTGTAAACAATGCTGGAAGCAGTT 633
QY 121 GACAAGTGTCCCATGTGC 138
Db 634 GACACGTGTNCCATGTGC 651

RESULT 14
BB489839
LOCUS
DEFINITION
ACCESSION
VERSION

BB489839 218 bp mRNA linear EST 23-JUL-2000
BB489839 RIKEN full-length enriched, 13 days embryo stomach Mus
musculus cDNA clone D530010E15 3' similar to U36842 Mus musculus
IAP homolog A (MIHA) mRNA, mRNA sequence.
BB489839
BB489839.1 GI:9407448

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# KEYWORDS SOURCE ORGANISM

EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 218)  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci  
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Itoh,M.,  
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,  
Izawa,M., Kaotera,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,  
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,  
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
Oono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata  
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,  
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya  
T., Tsunoda,I., Watanabe,A., Watanabe,S., Yamamura,T., Yamazaki,I.,  
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino  
M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
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The Institute of Physical and Chemical Research (RIKEN)  
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Fax: 81-45-503-9216  
Email: genome-res@gs.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermotabilization and thermoactivation of thermostable enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

# TITLE JOURNAL COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermotabilization and thermoactivation of thermostable enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

# FEATURES source

1. .218  
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/db\_xref="taxon:10090"  
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/dev\_stage="13 days embryo"  
/lab\_host="DH10B"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN, Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5',  
GAGGAGAGAGCGCGCCGACTCGAGTCTTTTCTTTTCTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5',  
GAGGAGAGATCTCGAGTCTTTTCTTTTCTTNN 3']. cDNA  
was cleaved with BamHI and XhoI. Vector: a modified  
pBluescript KS(+) after bulk excision from Lambda FLC I."  
61 a 52 c 38 g 67 t  
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Best Local Similarity 89.1%; Pred. No. 1.3e-24;  
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Qy 121 GACAAGTGTCCCATGTGC 138  
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RESULT 15  
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LOCUS AG124597 684 bp DNA linear GSS 04-NOV-2001  
DEFINITION Pan troglodytes DNA, clone: PTB-134J15.F, genomic survey sequence.  
ACCESSION AG124597  
VERSION AG124597.1 GI:16653762  
KEYWORDS GSS.  
SOURCE BAC Library clone: PTB-134J15.F.  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Tokoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB  
Unpublished  
TITLE 2 (bases 1 to 684)  
JOURNAL  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Tokoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimb@gs.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library PTB this BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
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/sex="male"  
/cell\_type="lymphoblast"  
/clone.lib="PTB Chimpanzee Male BAC Library"  
BASE COUNT 216 a 143 c 149 g 176 t  
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Query Match 82.6%; Score 114; DB 17; Length 684;  
Best Local Similarity 89.1%; Pred. No. 1.9e-24;  
Matches 123; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
Qy 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60  
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Qy 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACATTTGTAACAATGCTGCTGAAGCAGTT 120  
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Db 407 GCTGTGTTTTTATTCTTCCTGCGACATCTGGTCACTTGTAAACAATGCTGCTGAAGCAGTT 466  
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QY 121 GACAAGTGTCCCATGTGC 138  
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Db 467 GACAATGTCCCATGTGC 484

Search completed: April 16, 2003, 00:55:01  
Job time : 664.292 secs